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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 00:48:08 ; Search time 9448.45 Seconds
(Without alignments)
17973.196 Million cell updates/sec

Title: US-09-778-516A-1
Perfect score: 8115
Sequence: 1 gatgcagcgccagatatcac.....gcgtgtcgtacgacgctc 8115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:
1: gb_ba:*
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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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1	3535	43.6	3660	1	LBAGAL	M23530 L. delbrueckii
2	3497.2	43.1	5059	6	AX009488	AX009488 Sequence
3	3386.6	41.7	5015	1	LBALACZBUL	M55068 L. delbrueckii
4	1336.4	16.5	3840	12	EVEI32038	AJ132038 Expressio
5	1307.4	16.1	11592	6	AX107924	AX107924 Sequence
6	1245.2	15.3	3853	6	BD009729	BD009729 Tissue sp
7	1240.4	15.3	3853	6	AR098190	AR098190 Sequence
8	1236.2	15.2	2093	1	LP1P1PRP	M1223 Plasmid plp
9	1191.6	14.7	2140	1	C300RFR	J03319 Plasmid pc3
10	1152.4	14.2	4699	12	AF346623	AF346623 RAGE vect
11	1148.2	14.1	14455	12	AF356044	AF356044 Sequence
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13	1082	13.3	5446	6	AX319694	AX319694 Sequence
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22	988	12.2	4597	6	AX060344	AX060344 Sequence
23	985.2	12.1	4276	6	AX154496	AX154496 Sequence
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ALIGNMENTS

RESULT	1	LBAGAL	3660 bp	DNA	linear	BCI 26-APR-1993
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DEFINITION	L. delbrueckii bulgaricus beta-galactosidase gene, complete cds.					
ACCESSION	M23530					
VERSION	M23530.1 GI:149546					
KEYWORDS	galactosidase.					
SOURCE	L. delbrueckii bulgaricus (strain B131) DNA.					
ORGANISM	Lactobacillus delbrueckii					
REFERENCE	1 (bases 1 to 3660)					
AUTHORS	Schmidt, B.F., Adams, R.M., Regnadt, C., Power, S. and Mainzer, S.E.					
TITLE	Expression and nucleotide sequence of the Lactobacillus bulgaricus beta-galactosidase gene cloned in Escherichia coli					
JOURNAL	J. Bacteriol. 171, 625-635 (1989)					
MEDLINE	89123132					
COMMENT	Draft entry and computer-readable sequence for [1] kindly submitted by B.F. Schmidt, 29-MAR-1989.					
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misc.feature 3477..3531
/note="region of dyad symmetry"
BASE COUNT 941 a 927 c 996 g 796 t
ORIGIN 1bp upstream of HindIII site.

Query Match 43.6%; Score 3535; DB 1; Length 3660;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 3590; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

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QY 4540 aagccgaattcgacacacatgcgcgctactaagtgatcgatccgaataaagttag 4599
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DB 70 -----CCGATTAATAAAGTTAGG 85
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QY 4600 cgaagcgttgccttggtgccaagcagcagcgttaaggtctacgcccatttgcgctatgct 4659
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DB 686 CTTCTATCAGAAAGCTTTGACGATGAGATTAATTAAGTCAGTCAAAAGTACCGGCAACT 745
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QY 5260 ggaactgcaagccttggcagccccagtatgccaagctccaatccaatggagcgagc 5319
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RESULT 2
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 ACCESSION AX009488
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 ORGANISM
 Lactobacillus delbrueckii subsp. bulgaricus.
 Lactobacillus delbrueckii subsp. bulgaricus
 Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 Lactobacillus.

REFERENCE 1 (bases 1 to 5059)
AUTHORS Brignon, P., Gendreau, F., and Benbadis, L.
TITLE Mutant *Lactobacillus bulgaricus* strains free from beta-galactoside
JOURNAL activity
Patient: WO 9961627-A 1 02-DEC-1999;
GERVAIS DANONE CO (FR); BRIGNON PIERRE (FR); GENDRE FRANCOIS (FR);
BENBADIS LAURENT (FR)
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ORIGIN

Query Match 43.1%; Score 3497.2; DB 6; Length 5059;
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LOCUS	EVEI32038 3840 bp mRNA circular SYN 28-JUL-1999
DEFINITION	Expression vector pCDPr.
ACCESSION	AJ132038
VERSION	AJ132038.1 GI:5640088
KEYWORDS	AMP gene; beta lactamase; ColeI origin of replication; multiple cloning site; Sp6 promoter; SV40 origin of replication; T7 promoter; xanthine-guanine phosphoribosyl transferase; Xanthine-guanine phosphoribosyl transferase gene.
SOURCE	Expression vector pCDPr.
ORGANISM	Expression vector pCDPr.
REFERENCE	artificial sequence; vectors.
AUTHORS	1 (bases 1 to 3840)
TITLE	Zeng,B.J.
JOURNAL	Mammalian Expression Vector for with fuse Xanthine-guanine phosphoribosyl transferase Tag
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 3840)
TITLE	Zeng,B.J.
JOURNAL	Direct Submission
REFERENCE	Submitted (27-FEB-1999) Zeng B.J., Gene Engineering Center,
TITLE	Institute of Microbiology, Zhongguancun, Beijing, Beijing 100080,
JOURNAL	CHINA
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OY	61 attacggaggtcattagttcattagcccataatagaggtccggttacctaaactaacgta 120	
Db	195 ATTACGGGGGTCAATTAAGTTTCATAGCCCATATATAGGAGTTCCGCTTACATACTTACGGGTA 254	
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Db	315 GTTCCCATAGTAAGTACCCCAATAGGAGCTTTCCATTGACCTCATGGGTGGAGCTATTATACG 374	
OY	241 taaactgcccacttggagagtaacaaatgataatgataatgacaaaggaagcccccattac 300	
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Db	615 ATTGACGTCAATAGGAGGAGTTTGTTTTGGACCAAAATTCACAGGGAGCTTTCCAAAATGTGT 674	
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OY	661 actcaactatagggaagcccaagcttggtaacggagctcgatcccaactagtaacggccgca 720	
Db	795 ACTCACTATAGGGAACCAAGCTTGGTACGAGCTCGGATTCACATTATTAACGGCGCGCA 854	

Oy	721	gtgtgctcggaattcttgaagatatacaatacaacacggtggagccgtctgagaatgatactaga-	773
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Oy	1106	ggggagagagcggttttcgcatattggagccttcccgcttccctgcacatgactgcgtcg	1155
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[illegible]

RESULT	5			
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LOCUS	AX107924	11592 bp	DNA	linear
DEFINITION	Sequence 52 from Patent WO0125466.			
ACCESSION	AX107924			
VERSION	AX107924.1	GI:13923307		
KEYWORDS	.			
SOURCE	synthetic construct.			
ORGANISM	artificial construct.			
REFERENCE	1 (bases 1 to 11592)			
AUTHORS	Slingsby,J., Kingsman,S.M., Rohll,J.O. and Slade,A.O.			

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Oy 1108 ggaagcggttgcgttctggttgcgtcttcgcgtcttcgcgtcttcgcgtcttcgcgt 1167
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RESULT 7

AR098190 LOCUS AR098190 3853 bp DNA Linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6074850.
ACCESSION AR098190
VERSION AR098190.1 GI:12807447
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 3853)
Antelman,D., Gregory,R.J. and Mills,K.N.
TITLE Retinoblastoma fusion polypeptides
JOURNAL Patent: US 6074850-A 5 13-JUN-2000;
FEATURES
source Location/Qualifiers
BASE COUNT 936 a 987 c 941 g 989 t
ORIGIN
Query Match 15.3%; Score 1240.4; DB 6; Length 3853;
Best Local Similarity 74.1%; Pred. No. 1.3e-283;
Matches 1911; Conservative 0; Mismatches 96; Indels 573; Gaps 4;
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Db 2670	GAATAAAAGGTCTCAAGAAAGATCTTTGATCTTCTTACGGGGTCTGACGCTCAGTGA 2729
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LOCUS	2093 bp DNA linear BCT 24-APR-1996
DEFINITION	plasmid plp1 (from lactobacillus plantarum CCM 1904) replication
ACCESSION	U01223
VERSION	M31223.1 GI:149684
KEYWORDS	replication protein.
SOURCE	Plasmid plp1 (tissue library: CCM 1904) DNA.
ORANISM	plasmids.
REFERENCE	1 (bases 1 to 2093)
AUTHORS	Bouis A., Brinquel, F., Frey, L., Kammerer, B., Belarbi, A., Guyonvarch, A. and Hubert, J. C.
TITLE	Structural organization of plp1, a cryptic plasmid from Lactobacillus plantarum CCM 1904
JOURNAL	Plasmid 22 (3), 185-192 (1989)
MEDLINE	90222315
COMMENT	Draft entry and computer-readable sequence for [1] kindly submitted by B. Kammerer, 11-JAN-1990.
location/Qualifiers	1..2093

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ORIGIN 1 bp upstream of HindIII site.

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RESULT 9
C30ORFR C30ORFR 2140 bp DNA linear BCT 07-MAR-1996
LOCUS
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DEFINITION Plasmid pc3011 (from L.plantarum) ORF R, complete genome.
ACCESSION J03319
VERSION J03319.1 GI:144180
KEYWORDS complete genome.
SOURCE Plasmid pc3011 DNA.
ORGANISM Plasmid pc3011
plasmids.
REFERENCE 1 (bases 1 to 2140)
AUTHORS Skagen,M.
TITLE The complete nucleotide sequence of a small cryptic plasmid from
Lactobacillus plantarum
JOURNAL Plasmid 22 (2), 175-179 (1989)
MEDLINE 90160873
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by M.Skagen, 19-NOV-1989.
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LOCUS AF346623 4699 bp DNA circular SYN 30-AUG-2001
DEFINITION RAGE vector PRIG20, complete sequence.
ACCESSION AF346623
VERSION AF346623.1 GI:15383986
KEYWORDS
SOURCE RAGE vector PRIG20.
ORGANISM RAGE vector PRIG20
REFERENCE
AUTHORS artificial sequence; vectors.
1 (bases 1 to 4699)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,E., Veloso,N., Kalka,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL 21227151
MEDLINE 11329013
PUBMED 2 (bases 1 to 4699)
REFERENCE Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
AUTHORS Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krasnoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Veloso,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J.
and Ducar,M.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2001) Althersys, Inc., 3201 Carnegie Ave.,
Cleveland, OH 44115, USA
FEATURES
SOURCE Location/Qualifiers
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BASE COUNT 1062 a 1363 c 1275 g 998 t 1 others
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Best Local Similarity 76.48; Pred. No. 1.1e-262;
Matches 1524; Conservative 0; Mismatches 356; Indels 74; Gaps 6;
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Db 2055 GATCTTACCTAGA 2068

RESULT 11
AX356044 14455 bp DNA linear PAT 06-FEB-2002
LOCUS AX356044/c
DEFINITION Sequence 15 from Patent WO0183729.
ACCESSION AX356044
VERSION AX356044.1 GI:18620606
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Nemerow,G.R., von Seggern,D.J. and Friedlander,M.
TITLES Vectors for ocular transduction and use thereof for genetic therapy
JOURNAL Patent: WO 0183729-A 15 08-NOV-2001;
Novartis AG (CH); The Scripps Research Institute (US); Nemerow,
Glen R. (US); Von Seggern, Daniel J. (US); Friedlander, Marcy
(US)

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source location/Qualifiers
1.14455
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BASE COUNT 3698 a 3271 c 3565 g 3921 t
ORIGIN

Query Match 14.1%; Score 1148.2; DB 6; Length 14455;
Best Local Similarity 95.5%; Pred. No. 1.3e-261;
Matches 1196; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

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RESULT 12
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LOCUS
DEFINITION Cloning vector pcdna32EO DNA.
ACCESSION X90639.1 GI:949972
VERSION
KEYWORDS cloning vector; expression vector; multiple cloning site; plasmid.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3986)
AUTHORS Peters, H., Hundhausen, T., Kroenke, M. and Marget, M.
JOURNAL A new small sized high-level eukaryotic expression vector
REFERENCE 2 (bases 1 to 3986)
AUTHORS Peters, H.
JOURNAL Direct Submission
TITLE Submitted (07-AUG-1995) H. Peters, Inst. f. Immunologie,
COMMENT Michaelistr. 5, D-24105 Kiel, FRG.
FEATURES
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DEFINITION Sequence 5 from Patent WO0181614.
ACCESSION AX319694
VERSION AX319694.1 GI:17901350
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (sites)
AUTHORS Leng, J.
JOURNAL Cell proliferation assay
PATENT: WO 0181614-A 5 01-NOV-2001;
Chemicon International (US)
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source
Location/Qualifiers
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AUTHORS	Antelman, D., Gregory, R. J. and Wills, K. N.	
TITLE	Tissue specific expression of retinoblastoma protein	
JOURNAL	Patent: JP 2001503638-A 4 21-MAR-2001;	
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XX
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XX WPI: 2000-026146/03.
DR P-PSDB: AAY53620, AAY53621.
XX
PT New mutant *Lactobacillus bulgaricus* strain lacking beta-galactosidase
PT activity useful for making fermented milk products, especially yoghurt
PT
XX
PS Disclosure; Page 15-22; 32pp; French.
XX
CC The present sequence represents a lactose operon of *Lactobacillus*
CC *bulgaricus*, and encodes a permease protein and beta-galactosidase
CC protein. The specification describes mutant *L. bulgaricus* strain lacking
CC beta-galactosidase activity, because it has a termination (nonsense)
CC mutation in at least one of the coding sequences of the lactose operon.
CC The resulting mutant strain is unable to ferment lactose. Since the
CC mutant strain cannot ferment lactose, fermented milk products produced
CC using it do not have to be cooled to prevent post-acidification. The
CC mutant *L. bulgaricus* strain of the invention is used for producing a
CC fermented milk product, especially yoghurt. Especially, milk is
CC fermented with a culture of the mutant strain and optionally
CC *Streptococcus thermophilus* in the presence of at least one sugar
CC assimilable by the mutant strain, preferably glucose.
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Db 3459 ttatctcagttgataacgctacgctacgcaatcggtccggttgagacttgcgcgtactaca 3518
OY 6624 cggcccttgaaaaataatccccactaccagggcggtcttcaatcttgagacttgaatgacaaag 6683
Db 3519 cggcccttgaaaaataatccccactaccagggcggtcttcaatcttgagacttgaatgacaaag 3578
OY 6684 gacttgaaaaaagacggcgacactgtcttatgtggggcgactcgaatgacggcgcaacggact 6743
Db 3579 gacttgaaaaaagacggcgacactgtcttatgtggggcgactcgaatgacggcgcaacggact 3638
OY 6744 atgaattctgvggaaacggcgctgtgtcttgcgtacccgagactgaatcgccgaaactggtca 6803
Db 3639 atgaattctgvggaaacggcgctgtgtcttgcgtacccgagactgaatcgccgaaactggtca 3698
OY 6804 atgtcaagcgctttagcccaacttaagttagaagtaaaagaatgggcaacttcttctca 6863
Db 3699 atgtcaagcgctttagcccaacttaagttagaagtaaaagaatgggcaacttcttctca 3758
OY 6864 aaaaacgaacatttatttaccacaacagctcacttactactcttgaactagcttcttgctcg 6923
Db 3759 aaaaacgaacatttatttaccacaacagctcacttactactcttgaactagcttcttgctcg 3818
OY 6924 atgtgcaagttgacctaccagaagcgcgctctgaacttggctcgtgagcctcgtgcgaatccg 6983
Db 3819 atgtgcaagttgacctaccagaagcgcgctctgaacttggctcgtgagcctcgtgcgaatccg 3878
OY 6984 ggaacttgcgcctgtgctgacggaagtcgctatgaaaaaggggaggtctgttaccggg 7043
Db 3879 ggaacttgcgcctgtgctgacggaagtcgctatgaaaaaggggaggtctgttaccggg 3938
OY 7044 taacggcccaacttaaaagaagacttgccttggcgagatgagggcttcaacttgcgtgaag 7103
Db 3939 taacggcccaacttaaaagaagacttgccttggcgagatgagggcttcaacttgcgtgaag 3998
OY 7104 cagaagaagtagtcaaaaagctgacggaatttaagccgggaagggcgccagatattgctg 7163
Db 3999 cagaagaagtagtcaaaaagctgacggaatttaagccgggaagggcgccagatattgctg 4058
OY 7164 atccgactacaacacttagagcctgaagaagataactccaattccttcttccaaagttca 7223
Db 4059 atccgactacaacacttagagcctgaagaagataactccaattccttcttccaaagttca 4118
OY 7224 aaggcttgccggttccctcctaagtatgcggttaggggaatacttgaagcggctgcggaat 7283
Db 4119 aaggcttgccggttccctcctaagtatgcggttaggggaatacttgaagcggctgcggaat 4178
OY 7284 ttacacttbgcgggcgcttgacgagacaacgacggggagtggtttacgctatgacttgg 7343
Db 4179 ttacacttbgcgggcgcttgacgagacaacgacggggagtggtttacgctatgacttgg 4238

OY 7344 cccggttggaaaaaatgcccgaagatagccccgtcttgaaaaaagacatcaagctgcgaagtaag 7403
Db 4239 cccggttggaaaaaatgcccgaagatagccccgtcttgaaaaaagacatcaagctgcgaagtaag 4298
OY 7404 aagaactcgttcttggtcaagaactgacctttagctgtgcctgtgcctttaaaggttgatttaa 7463
Db 4299 aagaactcgttcttggtcaagaactgacctttagctgtgcctgtgcctttaaaggttgatttaa 4358
OY 7464 ccgtgacctatgaagtcgatacgaagcggggcaagatttgcgtgaacaagcttgacttcccaggcg 7523
Db 4359 ctgtgacctatgaagtcgatacgaagcggggcaagatttgcgtgaacaagcttgacttcccaggcg 4418
OY 7524 cgggaagaagctgtgtcccttccagccttgccttggaaccccgcccgccgaagaactga 7583
Db 4419 cgggaagaagcggtctcccttccagccttgccttggaaccccgcccgccgaagaactga 4478
OY 7584 ccgattacgctactatgctgtcgtggacctaaagagactaacccaacggcttggaaagta 7643
Db 4479 ccgattacgctactatgctgtcgtggacctaaagagactaacccaacggcttggaaagta 4538
OY 7644 attacttgggcatctaccagggagcggttaaaaaagaacttgaacctata---tcgtccgc 7700
Db 4539 attacttgggcatctaccagggagcggttaaaaaagaacttgaacctatactgtccgc 4598
OY 7701 aggaacggggcaacccggaagaagttcgcgtgtacacagcctttagtgaagaaggcggt 7760
Db 4599 aggaacggggcaacccggaagaagttcgcgtgtacacagcctttagtgaagaaggcggt 4658
OY 7761 tggaaattacgyccaatgvgggcgagacttgaacttgcgttgccttgcataatctgcgcgcc 7820
Db 4659 tggaaattacgyccaatgvgggcgagacttgaacttgcgttgccttgcataatctgcgcgcc 4718
OY 7821 aaattgaagagcgagacacagcctttagaactgaactaaactaacacttgggttaagacct 7880
Db 4719 aaattgaagagcgagacacagcctttagaactgaactaaactaacacttgggttaagacct 4778
OY 7881 taagcccccagatcgggggtctgcgcggagatgactccttggggcgagaaaggtccacccggaat 7940
Db 4779 taagcccccagatcgggggtctgcgcggagatgactccttggggcgagaaaggtccacccggaat 4838
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Db 4839 tctgcctgtagtctcaaaaagcccgccagcttcgcctgctgtgattcagcccccttactaa 4898
OY 8001 aataaatgtcacattgacttaacagatgaatttttagraaaaaagaaagcggttagga 8060
Db 4899 aataaatgtcacattgacttaacagatgaatttttagraaaaaagaaagcggttagga 4958
OY 8061 agatggcaacgatacagaagtgacaaagcgagccggtgtcgtctagcgacggt 8114
Db 4959 agatggcaacgatacagaagtgacaaagcgagccggtgtcgtctagcgacggt 5012

RESULT 2
AA006760
ID AA006760 standard; DNA; 3203 BP.
XX
AC AA006760;
XX
DT 25-FEB-1991 (first entry)
XX
DE Sequence of beta-galactosidase gene.
XX
KW pBR329; pBG1; ds.
XX
OS Lactobacillus bulgaricus S870034.
XX
FH Key Location/Qualifiers
FT 285..3083
FT CDS /*tag= a
XX
PN JP02261383-A.

XX 24-OCT-1990.
XX 31-MAR-1989; 89JP-0082851.
XX 31-MAR-1989; 89JP-0082851.
XX (SNOW) SNOW BRAND MILK PRODUCTS.
XX WPI: 1990-364398/49.
XX P-PSDB: AAR08132.
XX
XX DNA from *Lactobacillus bulgaricus* SFB0034 encoding beta-
XX galactosidase - used to produce high yields of beta-galactosidase by
XX recombinant DNA technology.
XX
XX Claim 1; Fig 1; 6pp; Japanese.
XX
XX Beta-galactosidase may be produced from an *E.coli* expression system
XX transformed by the gene sequence incorporated in the plasmid vector
XX pBcl, derived from pBR329.
XX
XX Sequence 3203 BP; 836 A; 807 C; 867 G; 693 T; 0 other;

Query Match 38.3%; Score 3110.6; DB 11; Length 3203;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3177; Conservative 0; Mismatches 14; Indels 8; Gaps 5;

QY 4920 cgatccgagccagcgtcccaagccctgtgagtgtatcttaagttgaaggaagattaga 4979
D 1 cgatccgagccagcgtcccaagccctgtgagtgtatcttaagttgaaggaagattaga 60
QY 4980 aaatgagcaataaagttagtaaaagaaaaaagattgaccagcgaccctgtgctga 5039
D 61 aaatgagcaataaagttagtaaaagaaaaaagattgaccagcgaccctgtgctga 120
QY 5040 ctgacccgggaagtttaagaagtcaataaattcccccgcactccgacatgagtcctcc 5099
D 121 ctgacccgggaagtttaagaagtcaataaattcccccgcactccgacatgagtcctcc 180
QY 5100 aagcccggaagaaatctgaggaaggaagcgaagtcagtttaagtcagtccttgaggagact 5159
D 181 aagcccggaagaaatctgaggaaggaagcgaagtcagtttaagtcagtccttgaggagact 239
QY 5160 ggcctgattgactgcgtgaaacacggccagggaccagtcacactctctatgcaagaacttg 5219
D 240 ggcctgattgactgcgtgaaacacggccagggaccagtcacactctctatgcaagaacttg 299
QY 5220 acgatagcaatttaagtcaatcaaatgtaacccggcaacctggaactgcaaggtcttgcc 5279
D 300 acgatagcaatttaagtcaatcaaatgtaacccggcaacctggaactgcaaggtcttgcc 359
QY 5280 agcccgatgataagtcagtcacataatcattgggacggagcgagagagatttccggccc 5339
D 360 agcccgatgataagtcagtcacataatcattgggacggagcgagagagatttccggccc 419
QY 5340 aaattccaagcaaaaatccgctcgtctctatgttcaagatacttgaacctgtgaagctt 5399
D 420 aaattccaagcaaaaatccgctcgtctctatgttcaagatacttgaacctgtgaagctt 479
QY 5400 tct-gggaaggaagtaagcttgaagtttgaagggcgagcaacagcattatgtctg 5458
D 480 tctggggaaggaagtaagcttgaagtttgaagggcgagcaacagcattatgtctg 539
QY 5459 ctgagacggccactctgtggtgaggaaggaagcctttacccaaggaattatggtt 5518
D 540 ctgagacggccactctgtggtgaggaaggaagcctttacccaaggaattatggtt 599
QY 5519 accaagttccccaagaaagaaataaacgcgctggaagtgtctctcaaatattctcc 5578
D 600 accaagttccccaagaaagaaataaacgcgctggaagtgtctctcaaatattctcc 659

QY 5579 gctcctggtcgtgaagaccagactctgctgacatgtctgttctgaagatacagtgact 5638
D 660 gctcctggtcgtgaagaccagactctgctgacatgtctgttctgaagatacagtgact 719
QY 5639 cttaagcccaagccgctctgctgacttggagacacttaagcttaagcccaagcttgaag 5698
D 720 cttaagcccaagccgctctgctgacttggagacacttaagcttaagcccaagcttgaag 779
QY 5699 aactaccaaaaagaaagcttgaagctgaagccaataatgctacacgcttgcacaatgccc 5758
D 780 aactaccaaaaagaaagcttgaagctgaagccaataatgctacacgcttgcacaatgccc 839
QY 5759 agctttagcgtgaagtgccggaatgataagtgagtgactgtgtctgaagaagctggccca 5818
D 840 agctttagcgtgaagtgccggaatgataagtgagtgactgtgtctgaagaagctggccca 899
QY 5819 atcagaagcgaagcagcgtgaagtaactcactctgctgatttggccagagctgagcgcg 5878
D 900 atcagaagcgaagcagcgtgaagtaactcactctgctgatttggccagagctgagcgcg 959
QY 5879 gaaaagcctaacccttaaccaggtccgctgtattataccaagcgaagcactcttagag 5938
D 960 gaaaagcctaacccttaaccaggtccgctgtattataccaagcgaagcactcttagag 1019
QY 5939 gtttagccgagcgaagtggtgttccgcgaacttgaactaaagacgggattatgactt 5998
D 1020 gtttagccgagcgaagtggtgttccgcgaacttgaactaaagacgggattatgactt 1079
QY 5999 aacgagcagcagcagctcttaagaaggggccaacccgcaagatttgcagtaagtgtgt 6058
D 1080 aacgagcagcagcagctcttaagaaggggccaacccgcaagatttgcagtaagtgtgt 1139
QY 6059 cgggctacacggaagagatataatgatctggaacataacgaacatgaaagcgaagcaacatc 6118
D 1140 cgggctacacggaagagatataatgatctggaacataacgaacatgaaagcgaagcaacatc 1199
QY 6119 aatgctgtccgctgtctcctacataccggaacacgctccttttcgggctctgagcaag 6178
D 1200 aatgctgtccgctgtctcctacataccggaacacgctccttttcgggctctgagcaag 1259
QY 6179 taaggccttaacgttcaattgaaagcttaaccttgaagccagcggcacttgggaaaaagt 6238
D 1260 taaggccttaacgttcaattgaaagcttaaccttgaagccagcggcacttgggaaaaagt 1319
QY 6239 ggggggacgaagaatcctagcttcaatgttccagggcgaatgacacgacttggctggagcc 6298
D 1320 ggggggacgaagaatcctagcttcaatgttccagggcgaatgacacgacttggctggagcc 1379
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D 1380 agcttattccgggtggaagaataatgagtgctgggaaacgaacatgcttaacttaac 1439
QY 6359 tggctttagcaatgagttcttaacggcgacacttcttggccaagtgagctgattacgct 6418
D 1440 tggctttagcaatgagttcttaacggcgacacttcttggccaagtgagctgattacgct 1459
QY 6419 cgggaagcgtgattccgacccgggttcaagcaatagaaggggtgacccaacccggaagttt 6478
D 1500 cgggaagcgtgattccgacccgggttcaagcaatagaaggggtgacccaacccggaagttt 1559
QY 6479 gacgagcgaacccaagattgaagcccggaatgatagtctccggccaaggttaattgaagatac 6538
D 1560 gacgagcgaacccaagattgaagcccggaatgatagtctccggccaaggttaattgaagatac 1619
QY 6539 ttgaccaataaacagccaagcattatctccagttgaatcgcgtccagccatgaggcaac 6598
D 1620 ttgaccaataaacagccaagcattatctccagttgaatcgcgtccagccatgaggcaac 1678
QY 6599 tccgtctgtagcctgtgccccttacaagcccttgaagaataatccccactacagggcgcc 6658
D 1679 tccgtctgtagcctgtgccccttacaagcccttgaagaataatccccactacagggcgcc 1736
QY 6659 ttcatctgagactgattgaccagaagcctggaagaagacgggcaactgtcttattagggcc 6718


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Db 1737 ttcattcgggactggttgcccaaggactgtgaaagaacggcgacccgtttatgtgggc 1796
QY 6719 gacttcgatacgcgcgcacacgactatgaattctgcgggaacggcctgtcttcgtgac 6778
Db 1797 gacttcgatacgcgcgcacacgactatgaattctgcgggaacggcctgtcttcgtgac 1856
QY 6779 cgcgcgatacgcgcgcacacgactatgaattctgcgggaacggcctgttcgcaactatgtaa 6838
Db 1857 cgcgcgatacgcgcgcacacgactatgaattctgcgggaacggccttcacgccaactatgtaa 1916
QY 6839 gtaaaagatgagcagctcttcctcaaaaacgacaattatattacacacgactatctac 6898
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QY 6899 tactcttgactagctcttcttgatgacatgacatgacacgacgacgacgacgacgac 6958
Db 1977 tactcttgactagctcttcttgatgacatgacatgacacgacgacgacgacgacgac 2036
QY 6959 ttgagcctgagacgcttgacacacgacacgacacgacacgacacgacacgacacgacac 7018
Db 2037 ttgagcctgagacgcttgacacacgacacgacacgacacgacacgacacgacacgacac 2096
QY 7019 gaaaaagggaggtcgcctacacggtgtaacgacgacacgacacgacacgacacgacac 7078
Db 2097 gaaaaagggaggtcgcctacacggtgtaacgacgacacgacacgacacgacacgacac 2156
QY 7079 gatgagggctcactgttgctgacgacgacgacgacgacgacgacgacgacgacgac 7138
Db 2157 gatgagggctcactgttgctgacgacgacgacgacgacgacgacgacgacgacgac 7216
QY 7139 ccggaagggcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 7198
Db 2217 ccggaagggcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 2276
QY 7199 ttccaaattctctcccaaggtcgaagggcgtgcggttccctcaagtaatgcggtgag 7258
Db 2277 ttccaaattctctcccaaggtcgaagggcgtgcggttccctcaagtaatgcggtgag 2336
QY 7259 gaattacttgaagggcgtgcggaattactcttcgacgacgacgacgacgacgacgacgac 7318
Db 2337 gaattacttgaagggcgtgcggaattactcttcgacgacgacgacgacgacgacgacgac 2396
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QY 7679 aacttaacgacacacacacacacacacacacacacacacacacacacacacacacacac 7735
Db 2757 aacttaacgacacacacacacacacacacacacacacacacacacacacacacacacac 2816
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Db 2817 cagctcttgatgaaagggcggtctggaattacgacgacgacgacgacgacgacgacgac 2876
QY 7796 tctgctttgacacatattctgcgcgcacacacacacacacacacacacacacacacacac 7855
Db 2877 tctgctttgacacatattctgcgcgcacacacacacacacacacacacacacacacacac 2936
QY 7856 aacaattacacttgggttaagccttaagcgcacacacacacacacacacacacacacacacac 7915
Db 2937 aacaattacacttgggttaagccttaagcgcacacacacacacacacacacacacacacacac 2996
QY 7916 tgggggcaagaaggtccacacgacacacacacacacacacacacacacacacacacacac 7975
Db 2997 tgggggcaagaaggtccacacgacacacacacacacacacacacacacacacacacacac 3056
QY 7976 ctggtgattacgacacacacacacacacacacacacacacacacacacacacacacacac 8035
Db 3057 ctggtgattacgacacacacacacacacacacacacacacacacacacacacacacacac 3116
QY 8036 ttgtaaaacgaagcgagtgaggaagatgcaacgacgacgacgacgacgacgacgacgac 8095
Db 3117 ttgtaaaacgaagcgagtgaggaagatgcaacgacgacgacgacgacgacgacgacgac 3176
QY 8096 gcgtgtcgtacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 8114
Db 3177 gcgtgtcgtacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 3195

RESULT 3
AAE83089
ID AAE83089 standard; DNA; 11592 BP.
XX
AC
XX
AAE83089;
XX
DT 29-JUN-2001 (first entry)
XX
DE
XX
E1AV expression vector pONT82a CMVhyb sequence.
XX
Retrovirus: recombinase recognition sequence; RRS; LTR; recombinase;
long terminal repeat; pharmaceutical; cytosolic; anti-inflammatory;
antirheumatic; antiarthritic; antisthmatic; osteopathic; cardiant; E1AV;
vaccinoprotective; neurotrophic; neurotrophic; cerodiprotective; antiporotic;
antiartherosclerotic; vulnary; anti-HIV; antilucer; thrombolytic;
dermatological; gene therapy; ss.
XX
OS
Synthetic.
XX
E1AV expression vector pONT82a CMVhyb sequence.
XX
WO200125466-A1.
XX
12-APR-2001.
XX
05-OCT-2000; 2000WO-GB03837.
XX
05-OCT-1999; 99GB-0023558.
XX
(OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Slingsby J, Kingsman SM, Rohll J, Slade A;
XX
WPI; 2001-281732/29.
XX
Modifying producer cells for making retrovirus by transfecting with a
long terminal repeat and 3'-recombinase recognition sequence, in presence
of recombinase -
XX
Examples: Page 111-114; 133pp; English.
XX
The invention relates to a method of modifying producer cells for making
retrovirus by transfecting with a construct comprising a 5'-recombinase
recognition sequence (RRS), long terminal repeat (LTR) and 3'-RRS, in
presence of recombinase. The regulated retroviral vector produced is
useful in the manufacture of a pharmaceutical composition to deliver a

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Db 9985 atccggaacaaaccacgcgtgtagcggtgtttttgtttgtagcagcagattac 10044
Qy 1883 gccgagaaaaaggtctcaagaagatccttgatcttttctacggggtctaacgtca 1942
Db 10045 gccgcagaaaaaaggatcctaagaagatccttgatcttttctacggggtctaacgtca 10104
Qy 1943 gtggaacgaaaaactcgcgttaagggatttggcatagcgcgatacatattgaatgat 2002
Db 10105 gtggaacgaaaaactcgcgttaagggatttggcatagatattatacaaaagatcttcac 10164
Qy 2003 ttaga 2007
Db 10165 ctaga 10169

RESULT 4
AAV40006 standard; DNA; 3853 BP.
XX
AC AAV40006;
XX
DT 15-FEB-1999 (first entry)
XX
DE Plasmid pCTM.
XX
KW E2F; transcription factor; human; retinoblastoma protein RB;
KW bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW peripheral vascular disease; therapy; plasmid pCTM; ss.
XX
OS Chimeric - cytomegalovirus.
OS Chimeric - mastadenovirus.
OS Chimeric - bacteriophage T7.
OS Chimeric - bacteriophage SP6.
OS Chimeric - rhesus macaque polyoma virus.
OS Chimeric - Bos taurus.
XX
FH Key Location/Qualifiers
FT Promoter 209..864 /tag= a
FT /note= "CMV promoter"
FT misc_feature 907..1131 /tag= b
FT /function= tripartite leader sequence
FT promoter 1132..1149 /tag= c
FT /note= "SP6 promoter"
FT misc_feature 1679..3853 /tag= d
FT /note= "pUC19 backbone H3 to AclI"
FT CDS complement (2857..3717) /tag= e
FT /note= "AMP-ORF"
XX
PN WO9821228-A1.
XX
PD 22-MAY-1998.
XX
PF 13-NOV-1997; 97WO-US21821.
XX
PR 14-FEB-1997; 97US-0801092.
XX
PR 15-NOV-1996; 96US-0751517.
XX
PA (CANI-) CANI INC.
XX
PI Antelman D, Gregory RJ, Willis KN;
XX
DR WPI; 1998-297858/26.
XX
PT New fusion polypeptide of, e.g. transcription factor - used to
PT treat, e.g. hyper-proliferative disease such as cancer and
PT restenosis
```

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XX
PS Example 1; Fig 4; 91pp; English.
CC This is the nucleotide sequence of pCTM, a plasmid which contains
CC a CMV promoter, a tripartite adenovirus leader flanked by T7 and
CC SP6 promoters, and a multiple cloning site with a bovine growth
CC hormone polyA site and downstream SV40 polyA site. It has been
CC used as a vector for the expression of fusion proteins of the
CC invention that comprise retinoblastoma protein (BP, see AM62465) and
CC E2F transcription factor (see AM62464). Such fusion proteins,
CC particularly expressed from gene therapy vectors, are used to treat
CC hyperproliferative conditions, specifically cancer (particularly of
CC the bladder) or restenosis. They are more effective in repressing
CC transcription of the E2F promoter than RB alone and cause
CC cell-cycle arrest in a variety of cells.
XX
SQ Sequence 3853 BP; 936 A; 986 C; 942 G; 989 T; 0 other;

Query Match 15.3%; Score 1245.2; DB 19; Length 3853;
Best Local Similarity 74.2%; Pred. No. 7e-177;
Matches 1914; Conservative 0; Mismatches 93; Indels 573; Gaps 4;

Qy 1 gatgtacgggccaagataatagcgttgacattgattatgactagttatattagtaatca 60
Db 210 gatgtacgggccaagataatagcgttgacattgattatgactagttatattagtaatca 269
Qy 61 ataacggggtcatattgattatagcccatatagattccgggttataacttaacgta 120
Db 270 ataacggggtcatattgattatagcccatatagattccgggttataacttaacgta 329
Qy 121 aatggccgcctgtgcacgcgcgaacgaccccgccattgtgcgtcaataatgacgat 180
Db 330 aatggccgcctgtgcacgcgcgaacgaccccgccattgtgcgtcaataatgacgat 389
Qy 181 gtcccatagtaacgccaataggacttccattgacgtcaatgggttgactattacg 240
Db 390 gtcccatagtaacgccaataggacttccattgacgtcaatgggttgactattacg 449
Qy 241 taaactggccactgtgcagacatcaagtgatcatatgccaatgacggcccatattgac 300
Db 450 taaactggccactgtgcagacatcaagtgatcatatgccaatgacggcccatattgac 509
Qy 301 gtaaatgacgttaaatggccgccttgacattatgccaatgacattatgacatt 360
Db 510 gtaaatgacgttaaatggccgccttgacattatgccaatgacattatgacatt 569
Qy 361 cctacttggcagtaacatcagtaattagtcacgtattacccaatgggttgattg 420
Db 570 cctacttggcagtaacatcagtaattagtcacgtattacccaatgggttgattg 629
Qy 421 catatacctaattggcggtgatagcggtttagtaccggaattccaagttccacccc 480
Db 630 catatacctaattggcggtgatagcggtttagtaccggaattccaagttccacccc 689
Qy 481 atgagcgtcaatggcggtgtgttttgaccaccaaatcaacggaattccaatgtcgt 540
Db 690 atgagcgtcaatggcggtgtgttttgaccaccaaatcaacggaattccaatgtcgt 749
Qy 541 aacaactcggcccatatgacgcaaatggcggtgtagcggtgtagcggtgtagctata 600
Db 750 aacaactcggcccatatgacgcaaatggcggtgtagcggtgtagcggtgtagctata 809
Qy 601 agcagagctctctggtaactagagaaccacacgtctactcgtgtatgaaataatag 660
Db 810 agcagagctctctggtaactagagaaccacacgtctactcgtgtatgaaataatag 869
Qy 661 actcactataggagaccacagctt----- 685
Db 870 actcactataggagaccacagcttgcgcggttacacctcttccgcacgtctgtcg 929
Qy 686 ----- 685
```

Db 930 cgaagccagcgtgttgcgcggttgaaggacaaactctccgcgtcttccagtaactc 989
QY 686 -----ggtaccgagctcgatccactagtaacggcgccggtgtgc 726
Db 990 ttggaatcggaaccgcgtccgcgaacggaactccgcgcgcgaaggaacttgagagt 1049
QY 727 tgaattctcgagataatccatccacactgagccgc-----tcgag 767
Db 1050 ccgcatccgacccggaatcggaanaactctccgagcgccgcgtcagcttagaagtaattccgcg 1109
QY 768 catgcatctgagagccctatctatagtgtaacctaaatgctagactcgctatcagc 827
Db 1110 taacataatcgatgggcctacttactatagtgtaacctaaatgctagactcgctatcagc 1169
QY 828 ctgcacgtgctcttactagttgcagcaccatcggttgcgtcccccgcgcgtctcctt 887
Db 1170 ctgcacgtgctcttactagttgcagcaccatcggttgcgtcccccgcgcgtctcctt 1229
QY 888 gaccctggaaggtgcacactcccaactgtcttctcttaataaalgaggaattgcatcgca 947
Db 1230 gaccctggaaggtgcacactcccaactgtcttctcttaataaalgaggaattgcatcgca 1289
QY 948 ttgctctgagtagtgatctattctatctgaggggtgaggggtgaggaagaagaggagga 1007
Db 1290 ttgctctgagtagtgatctattctatcttctgaggggtgaggggtgaggaagaagaggagga 1349
QY 1008 ggaattggaagacacatagcaagcactgctgagga----- 1040
Db 1350 ggaattggaagacacatagcaagcactgctgagga----- 1409
QY 1041 ----- 1040
Db 1410 atttcgaattccaccgcgcgtctctatgaagaagtgtggtctcgaaatcgtttccggagcg 1469
QY 1041 ----- 1040
Db 1470 ccggtctgagtagtccctccagcgcgggagatctcattgctgaggttcttcgccaccaccaact 1529
QY 1041 ----- 1040
Db 1530 tgttattgcagcttaataatgtaataaataagcaataagcatcacaaatttccaaata 1589
QY 1041 ----- 1040
Db 1590 aagcatttcttccacgtcatctagttggtgttgcaccaatcacaatgtaattatc 1649
QY 1041 ----- 1040
Db 1650 atgtcgtatcacgtcgcacctagctagagcttggtgtaataatgtaattatcttctc 1709
QY 1041 ----- 1040
Db 1710 ctgtgtgaatattgtatccgtctcaatctccacacaacatacgacggagcaataaagt 1769
QY 1041 -----tgcggtgggtctatggs 1057
Db 1770 gtaaaagcctgggtgctgaatgagtgagtaactcacatattgctgctgcgtccacgcgc 1829
QY 1058 ctctct-----gaggcggaagaagaaccagctgcatltaatgaatcggaacgcgcgcg 1107
Db 1830 ccggttccagctcggaacactgtcgtgcagcgtcatltaatgtaatcggaacgcgcgcg 1889
QY 1108 ggaagagcggttctgcatctgagcgcctctccgctccgcgtcactgactcgctgcgt 1167
Db 1890 ggaagagcggttctgcatctgagcgcctctccgctccgcgtcactgactcgctgcgt 1949
QY 1168 cggtcgttccgctcgagcggtatcagctcctcaaaagcggttaataaggttatcca 1227
Db 1950 cggtcgttccgctcgagcggtatcagctcctcaaaagcggttaataaggttatcca 2009
QY 1228 cagaatacagggatacaacgcaagaagaacatgtagcaaaagcgcaagga 1287
Db 2010 cagaatacagggatacaacgcaagaagaacatgtagcaaaagcgcaagga 2069

QY 1288 accgtaaaagggccgcgttctggtcggttttccataaggtccgcgcgcgcctgacagcagc 1347
Db 2070 accgtaaaagggccgcgttctggtcggttttccataaggtccgcgcgcgcctgacagcagc 2129
QY 1348 acaaaaatcgacgtctcaagtcagagagtgtagcgaaccccgacagagataaagaatacagg 1407
Db 2130 acaaaaatcgacgtctcaagtcagagagtgtagcgaaccccgacagagataaagaatacagg 2189
QY 1408 cgttcccccctggaagctccctcgtgcgtccctcgttctccgaacccctgacagcagcag 1467
Db 2190 cgttcccccctggaagctccctcgtgcgtccctcgttctccgaacccctgacagcagcag 2249
QY 1468 accgtccgccttctccctccctccggaagcggtgcgtcttctccaatgctcagcagcagc 1527
Db 2250 accgtccgccttctccctccctccggaagcggtgcgtcttctccaatgctcagcagcagc 2309
QY 1528 atctcagttcggtgtagtgcgttccgcacagctggagctgtgtgacgaaccccccgttc 1587
Db 2310 atctcagttcggtgtagtgcgttccgcacagctggagctgtgtgacgaaccccccgttc 2369
QY 1588 agcccgacgcgtgcgtcttccggtatcagctgcttgaagtcacacccggtgaagacag 1647
Db 2370 agcccgacgcgtgcgtcttccggtatcagctgcttgaagtcacacccggtgaagacag 2429
QY 1648 acttatcgccactgtagcagcagccactgtagaagagatlaagcagagcgaggtatgtaggcg 1707
Db 2430 acttatcgccactgtagcagcagccactgtagaagagatlaagcagagcgaggtatgtaggcg 2489
QY 1708 gtgtctacagagttcttgaagtgtgtgccttaactacagctacacacagaaagacagatttg 1767
Db 2490 gtgtctacagagttcttgaagtgtgtgccttaactacagctacacacagaaagacagatttg 2549
QY 1768 gtatctgcgtctgtgtaagccagttactcctcggaanaagttgtagtcttgcagcgcg 1827
Db 2550 gtatctgcgtctgtgtaagccagttactcctcggaanaagttgtagtcttgcagcgcg 2609
QY 1828 gcaaacacaacccgcgtgtagcgtgtgtttttgttgcgaagcagcagattacgcgcga 1887
Db 2610 gcaaacacaacccgcgtgtagcgtgtgtttttgttgcgaagcagcagattacgcgcga 2669
QY 1888 gaanaaaagagatccaaagagatccttgaatcttcttcttgaaggggttcggaagcagtgga 1947
Db 2670 gaanaaaagagatccaaagagatccttgaatcttcttcttgaaggggttcggaagcagtgga 2729
QY 1948 acgaaaactcaggttaagggatlttgtaatgtagcaggaatacatattgtaattgata 2007
Db 2730 acgaaaactcaggttaagggatlttgtaatgtagcaggaatacatattgtaattgata 2789

RESULT 5
AAA53878
ID AAA53878 standard; DNA: 5306 BP.
XX
AC AAA53878;
DT 03-JAN-2001 (first entry)
XX
XX Expression vector pRIG-22.
DE
XX vector: endogenous gene; activation: over-expression;
KW erythropoietin; growth hormone; drug discovery;
KW granulocyte colony stimulating factor; ds.
XX
OS Synthetic.
XX
PN W0200049162-A2.
XX
PD 24-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US04429.
XX
PR 19-FEB-1999; 99US-0253022.

PR 08-MAR-1999; 99US-0263814.
PR 26-MAR-1999; 99US-0276820.
XX
XX (ATHE-) ATHERSYS INC.
XX
XX Harrington JJ, Sherf B, Rundlett S;
XX
XX MPI; 2000-549276/50.
PT Non-targeted activation of endogenous genes, e.g. for the production of
PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
XX proteins and for drug discovery
XX
PS Disclosure; Fig 35; 240pp; English.
XX
XX New methods, vectors and cells are described for non-targeted
XX activation and over-expression of endogenous genes. The vector
XX constructs comprise transcriptional regulatory sequences (TRS) and
XX unpaired splice donor sequences (USDs), preferably the vectors
XX comprise (in sequential order) a TRS, an USDs, a rare cutting
XX restriction site (RCRS) and a linearization site (LS) with a second
XX TRS linked to a selectable marker (SM) lacking a polyadenylation
XX signal. The methods, vectors and cells comprising the vectors may
XX be used for the non-targeted activation and over-expression of
XX endogenous genes, e.g. for the production of proteins (including
XX erythropoietin, growth hormone or granulocyte-colony stimulating
XX factor) and drug discovery. The advantage of these methods are that
XX endogenous genes including those associated with human disease and
XX development, may be activated and isolated without prior knowledge
XX of the sequence structure, function or expression profile of
XX the genes being known.
SQ Sequence 5306 BP; 1303 A; 1365 C; 1383 G; 1255 T; 0 other;
Query Match 14.2%; Score 1152.4; DB 21; Length 5306;
Best Local Similarity 76.4%; Pred. No. 4.3e-163;
Matches 1524; Conservative 0; Mismatches 396; Indels 74; Gaps 6;
QY 23 gtggaattgatatgactgactgattatataagtaactaataaagggtgacttattgata 82
DB 140 gtggaattgatatgactgactgattatataagtaactaataaagggtgacttattgata 199
QY 83 gccacataatgaggttccggttaccataacttaacgttaaatggccgcctggctgaccgc 142
DB 200 gccacataatgaggttccggttaccataacttaacgttaaatggccgcctggctgaccgc 259
QY 143 ccaacgaccccgcccatgacgttcaataatgacgtatgttcccatagtaacgccaatag 202
DB 260 ccaacgaccccgcccatgacgttcaataatgacgtatgttcccatagtaacgccaatag 319
QY 203 ggaacttccattgacgtcaatggttgactatttaacgttaactggccacttggcagttac 262
DB 320 ggaacttccattgacgtcaatggttgactatttaacgttaactggccacttggcagttac 379
QY 263 atcaagtgtatcatatgacgaagtcgcccctattgacgtcaatgacgttaaatggccg 322
DB 380 atcaagtgtatcatatgacgaagtcgcccctattgacgtcaatgacgttaaatggccg 439
QY 323 ccttgacattatgccagtaacgttaatggaacttccacttggcagttacattacg 382
DB 440 ccttgacattatgccagtaacgttaatggaacttccacttggcagttacattacg 499
QY 383 tatatgatacgtatattacatggtgattggtgttggcagtaacatagggcgtgagat 442
DB 500 tatatgatacgtatattacatggtgattggtgttggcagtaacatagggcgtgagat 559
QY 443 agcggttggactaacgggattcccaagtcacaccccatgacgtcaatggagttgt 502
DB 560 agcggttggactaacgggattcccaagtcacaccccatgacgtcaatggagttgt 619
QY 503 tttagcacaataatcaacgggacttccaaatgtcgttaaacat-----ccgcgcc 554
|||||

DB 620 tttagcacaataatcaacgggacttccaaatgtcgttaaacatgtcgtccgcgcc 679
QY 555 attgacgcaaatggcggtgagtcgtgtacggtgggaggttataagcagaactctctg 614
DB 680 gttagcagaatggcggtgagtcgtgtacggtgggaggttataagcagaactctctg 739
QY 615 gctaactagaagaacccactgacttactgtactatcgaaatataacactacatataggga 674
DB 740 agtgaacgcgtacagatcatcacttaattctgacgaactactacgtataacgcgtacagcctcc 759
QY 675 gaccacagcttggtagcagagctcgatccacgtacgaagcgccagtgctgtg-gaatt 733
DB 800 tgcagaactgtcttagtgacaactatcgattccacacatatacagacgcagatgtaatt 859
QY 734 ctgcagatatcatcatcacatcgcgccgctcgagatgcatctacagggccattctat 793
DB 860 gtcaacagcgcattatgacgtacgtccgggagacagaacgcccccacatggctgagtaata 919
QY 794 agtgcacctaataatgtagagctcgctgtacgaacctcgactgtgcttctagttgcagc 853
DB 920 cgactcactatagggcgacagcggtgagtaactcgacttaagaagag----- 965
QY 854 catctgtgttggccctcccgctgcttcccttgacccttggaaggtgccaatcccaatg 913
DB 966 -----gctatctgcccagttagcagtcgagaagaagat 1000
QY 914 tcccttccataataatgaggaattgacatcgatgtctgagtaagtgatcatctatc 973
DB 1001 ttaagagagcggaaacaaacagcgtcaatgagccgaagtggcgagccgattcccatcg 1060
QY 974 tgggggtgggtgggcaagagacgaaggggagagattggagagaacatagcagcagatg 1033
DB 1061 gtatgttcgagatataagagccagcaacccactgtgctgcgtgtgagtcgcgcagc 1120
QY 1034 ctgggagatcggttgggtctctatgtcttgaaggcgaagaacacagctgacatgaat 1093
DB 1121 atgcg-----tccggtgtagagatcccaagcagcagtggtgtgctgcataga 1166
QY 1094 cggcccaacgcggggagagagcggttggctatgtggcgcttccgcttccctgcac 1153
DB 1167 tccggttagtgcagtagtggctccaagtacgaagcgaagcagactggcgcgccaagc 1226
QY 1154 tgaatcgctgcgtcgctgtctgttcggctgcggcgaggtatccatccacaaagcggt 1213
DB 1227 ggtcgcagagtggtctcg-agaaacggttgccatagaaatgtctcaacgatatagcgct 1285
QY 1214 aatacgttatccacagaatcagggagtaaacgcaggaagaacatgtgacaaagccca 1273
DB 1286 agatcctgtgtagtgcagagatctgtcgaagc-----catgtgacaaagccca 1334
QY 1274 gcaaaaggccaggaacccgttaaaaggccggttggctgttccataggtctcgccc 1333
DB 1335 gcaaaaggccaggaacccgttaaaaggccggttggctgttccataggtctcgccc 1394
QY 1334 cccctgaagcagcatcacaaataatcgacgtcacaatcgagagtgcggaaccccgacagact 1393
DB 1395 cccctgaagcagcatcacaaataatcgacgtcacaatcgagagtgcggaaccccgacagact 1454
QY 1394 ataaagatacagaggttcccccctggaaagctccctcgtgtgcctctcttccgaacct 1453
DB 1455 ataaagatacagaggttcccccctggaaagctccctcgtgtgcctctcttccgaacct 1514
QY 1454 ggcgcttacaggaatcgttcgccccttcccttcgggaaggtggcgcttccataag 1513
DB 1515 ggcgcttacaggaatcgttcgccccttcccttcgggaaggtggcgcttccataag 1574
QY 1514 ctcaacgtgtagtatctcaatcggttgcgttgcgttcgtcccaacgtggctgtgtga 1573
DB 1575 ctcaacgtgtagtatctcaatcggttgcgttgcgttcgtcccaacgtggctgtgtga 1634
QY 1574 cgaaccccgcttcaacgcgaacgcgtgcgcttatcccgtaactatcgtcttgaagtcaca 1633
DB 1635 cgaaccccgcttcaacgcgaacgcgtgcgcttatcccgtaactatcgtcttgaagtcaca 1694

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XX 1634 ccggaagacacactatcgccactgagcagcagcactgtatacagattagcagc 1693
DB 1695 ccggaagacacactatcgccactgagcagcagcactgtatacagattagcagc 1754
QY 1694 gaggatgtagggcggtctacagagcttctgaagtgtgacctactacagcactag 1733
DB 1755 gaggatgtagggcggtctacagagcttctgaagtgtgacctactacagcactag 1814
QY 1754 aagacagattgtgtatctgcgtctgctgaagccagttacccctggaaaaagattgg 1813
DB 1815 aagacagattgtgtatctgcgtctgctgaagccagttacccctggaaaaagattgg 1874
QY 1814 tagctctgtagccggaacaaacacacgcgtgtagcggtgtttttgtttgcaagca 1873
DB 1875 tagctctgtagccggaacaaacacacgcgtgtagcggtgtttttgtttgcaagca 1934
QY 1874 gcaatatacgcgcagaaaaaagatctcaagaagatcccttgcattcttcaagggtc 1933
DB 1935 gcaatatacgcgcagaaaaaagatctcaagaagatcccttgcattcttcaagggtc 1994
QY 1934 tgacgctcagtgagacaaacacacgcttaagagatttgctatgagcagatacat 1993
DB 1995 tgacgctcagtgagacaaacacacgcttaagagatttgctatgagcagatacat 2054
QY 1994 tgaatgtattaga 2007
DB 2055 gatcttcacactaga 2068

RESULT 6
AAV32374/c
ID AAV32374 standard; DNA: 14455 BP.
XX
AC AAV32374;
XX
DT 29-SEP-1998 (first entry)
DE Complete sequence of the pEI/Fiber plasmid.
XX
KM Circular; adenovirus type 5; pEI/Fiber plasmid; structural protein;
KM complementation; fiber protein; gene therapy; HIV; tumour; AD5;
KM early gene; Huntington's disease; May-Sachs disease;
KM sickle cell disease; El regulatory protein; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1460..4998
FT /tag- a
FT /note= "AD5 El regulatory gene"
FT complement (10922..14233)
FT /tag- b
FT /note= "AD5 fiber gene consisting of a CMV
FT promoter at 5' end of this gene"
XX
XX WO9813499-A2.
XX
XX 02-APR-1998.
XX
XX 24-SEP-1997; 97WO-EP05251.
XX
XX 25-SEP-1996; 96US-0719806.
XX
XX (NOVS ) NOVARTIS AG.
XX (SCRI ) SCRIPPS RES INST.
XX
XX Memerow GR, Von Seggern DJ;
XX
XX WPI; 1998-230709/20.
XX
XX Adenoviral vectors - which lack DNA encoding for structural protein
XX or fibre protein used particularly for gene therapy
PT

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XX
PS Example 1; Pages 112-131; 170pp; English.
XX
CC The present sequence is that of a pEI/Fiber plasmid used in the
CC method of the invention. The plasmid contains an adenovirus type 5 (AD5)
CC fiber gene controlled by a CMV promoter, an AD5 El gene and a pMAM
CC backbone. The invention provides adenoviral vectors having deletions of
CC all or part of various gene sequences encoding adenoviral structural
CC proteins and/or early region proteins. Deletions in these proteins would
CC allow a reduced risk of wild-type virus contamination and would also
CC allow packaging of foreign DNA in such vectors for a variety of
CC diagnostic and therapeutic applications. The adenoviral vectors having
CC deletions in the structural and/or early gene regions are produced by
CC cellular complementation of these adenoviral genes. Therefore, the
CC pEI/Fiber plasmid was used as a complementation plasmid which was
CC introduced into a host cell line where parts of the fiber and El gene
CC region would be stably inserted into the host cell chromosomes. The
CC resulting El/fiber gene deficient plasmid can be used as a gene delivery
CC vector. The vectors can be used for diagnosis or gene therapy, e.g. for
CC treating conditions characterised by hyper-proliferative cells (e.g.
CC tumours), genetic diseases (e.g. Huntington's disease, Tay-Sachs disease,
CC or sickle cell disease), or infections (e.g. HIV infection). They can
CC also be used for in vitro production of biologically active proteins.
XX
SQ Sequence 14455 BP; 3698 A; 3271 C; 3565 G; 3921 T; 0 other:

Query Match 14.1%; Score 1148.2; DB 19; Length 14455;
Best Local Similarity 95.5%; Pred. No. 1.6e-162;
Matches 1196; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

QY 755 gggcgccgtagcagatcagatcagagccctatctatagtgaccataatgctag 814
DB 11236 GCGGCCGCTCGAGCATGCATCTAGAGGCCCTATTCTATAGTGTACCTAATCTCTAG 11177
QY 815 ctgcgtatagcctgacgtgctgcttgccttgcctgagccagcactggtgttggccccc 874
DB 11176 CTGCGTGTACGCTCTGACGTGTGCTTCTTGTTCACACCATCTGTTGTGGCCCTTCCC 11117
QY 875 ccgtgcttcccttgacctggaagggtgccaactcccaactgcttctcctaataaagtgg 934
DB 11116 CCGGCGCTTCTTGTACCTGTGAGAGTGCGACTCCCACTGCTCTTCTTAATTAATGAGG 11057
QY 935 aaattgcagcattgtctgtagtgatcattctatctgagggtggtgggtggcagg 994
DB 11056 AAATGTGATCCCATGTTCTGTAGTGTGCTCATTTCTTGTGGGGGTGGGGTGGGAGG 10997
QY 995 acagcaaggaggagattgggaagaacataagcagcactgctggggatgagcgtgagccta 1054
DB 10996 ACAGCAAGGGGAGGATTGGGAACATAGCAGGCAATGCTGCGGATGCGGTGGCTCTTA 10937
QY 1055 tggcttctgaggcggaagaacacagctgcaattaaatgacgcggaacgctggggagag 1114
DB 10936 TGGCTTCTGAGGCGGCTA-----TGGGCTGTGAATATACCGACAGATGCTGAAGAG 10886
QY 1115 cggtttcgctattggtgctcttcgcgttctgctacagtcgcgtgctgctgctgt 1174
DB 10885 AAAATACCGATTCAGGGCGCTCTTCGCTTCCTCTCCTCATCTACGCTGCGCTGGCTGT 10826
QY 1175 tcgctcgcgcgcagcgcgtatagctcaactcaaaagcggtatacagttatccagagatc 1234
DB 10825 TCGGCTGCGGCGAGCGGATATAGCTCATCAAAAGCGGTATATACGGTTATCATCAGATTC 10766
QY 1235 aggggataacgcagaaagaacatgtgagcaaaagcagcaaaagccagaaacgttaa 1294
DB 10765 AGGGGATATACCGAGAAAGAAATGTAGTGAAGCAAAAGCCAGCAAAAGCCAGAACCTGTA 10706
QY 1295 aaagcgcggtgtgctggtgttttccataggtctgcgcgcgcctcagcagatcaacaaa 1354
DB 10705 AAAGGCGCGTGTGCGGTTTTCATATAGCTCCGCCCCCTGACGAGCATCACAAAAA 10646
QY 1355 tcgagctcgaagtgaaggtggtggaacccgacagagactataaagataccaggggtttcc 1414

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Db 10645 TCAGAGCTCAAGTAGAGGTGGGAAAAACCGACAGACGACTATMAAGATACAGAGCGGCTTCC 10586
QY 1415 cccgggaagctccctcgctgcgtcctcgttccgacctgcgcttaccgatacctgctc 1474
Db 10585 CCCTGGAGAGCTCCCTGCTGCGCTCTCCTGTTCCGACCCCTGCGGTTACCGGATACCTGTC 10526
QY 1475 cgccttctccctcgggaaagcgtgacgttctcctcaatgctcagcgtgtagtactcag 1534
Db 10525 CGCCTTCTCCCTTCGGGGAAGCGGTGGCGCTTTCATCATAGCTACAGCTGATGATCTCAG 10466
QY 1535 ttgggtgtagtgcgtgcgtcccaagctggtgctgtgtgcgaacccccgctcagccga 1554
Db 10465 TTTCGGTGAAGTCTGCTGCTCCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGA 10406
QY 1595 ccgctgacgttaccggttaactatgcttctgtagtccaaacccggttaagaacgactatc 1654
Db 10405 CCGCTGCGCCTTATCCGATACATATGCTGTGAGTCCAAACCGGTTAAGACACGACTTATC 10346
QY 1655 gccactgacagcagccactgtagaagattagacagagcgagtatgtagcggtgctac 1714
Db 10345 GCCACTGGACAGCACCTGCTAGACAGATTAGCAGACGAGTATGTAGCGGCTGCTAC 10286
QY 1715 agagttcttgaagtgtggtcctaactaaggctactagaagaagcaaglatgtgctcgt 1774
Db 10285 AGAGTTCTTAAGTGTGGCTTACTACTACGCTACACTAGAAAGACAGTATTTGCTATCTG 10226
QY 1775 cgcctcttgaagcaagttactccttcggaagaagttgtagtgccttgcgtcgtcaaca 1834
Db 10225 CGCCTCTCTAAGCAAGCACTTACCTTCGAAAAAGAGTTGTAAGCTTGTGATCCGGCAACA 10166
QY 1835 aaccacgcgtgtagcggtgtgttcttctgttgcgaagcagaactaagcgcaaaaaa 1894
Db 10165 AACACAGCGCGTAGCGGTGTTTGTGTTGCAACAGACAGATTACGCGCAGAAAAA 10106
QY 1895 aggaatcgaagaagatcccttgcattcttctcgaagggtctgcagcgtcaagtggaaacga 1954
Db 10105 AGGATTCACGAAGAGATCTTGTGATCTTCTACGCGGCTGTGACGCTCAGTGAACGAAA 10046
QY 1955 ctacagttgaaggattgtgcatagtagcgatatacatttgaaatgtagttaga 2007
Db 10045 CTCACGTTAAGGAGTTTGTGTCATGAGATTATCAAAAAAGATCTTCACTAGA 9993

RESULT 7
AAA59050/c
ID AAA59050 standard; DNA: 14455 BP.
XX
AC AAA59050;
XX
DT 07-NOV-2000 (first entry)
XX
DE Nucleotide sequence of the EI/fiber-expressing plasmid pEI/fiber.
XX
KW Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
EI gene; fiber gene; ss.
XX
OS Synthetic.
OS Adenovirus type 5.
XX
PN WO200042208-A1.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000MO-EP00265.
XX
PR 14-JAN-1999; 9905-0115920.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (SCRI) SCRIPPS RES INST.
XX
PI Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;
Skripchenko Y;

XX
DR MPI; 2000-476068/41.
XX
PT New nucleic acid comprising an adenovirus tripartite leader nucleotide
PT for producing high-capacity and targeted vectors for adenovirus-based
PT gene therapy -
XX
PS Example 1; Page 160-164; 212pp; English.
XX
CC The specification describes a nucleic acid molecule comprising an
CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
CC comprising two different TPL exons or three same or different TPL
CC exons. The nucleic acid is used to produce an adenovirus vector particle,
CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
CC vectors, target an adenovirus vector to a cell, produce a modified
CC adenovirus, deliver a heterologous gene to an animal and produce a
CC gutless adenoviral vector particle. The present sequence represents
CC a EI/fiber-expressing plasmid, which was used for complementation of
CC EI/fiber-gene deleted adenoviruses.
XX
SQ Sequence 14455 BP; 3698 A; 3271 C; 3565 G; 3921 T; 0 other:

Query Match 14.1%; Score 1148.2; DB 21; Length 14455;
Best Local Similarity 95.5%; Pred.No.1.6e-162;
Matches 1196; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

QY 755 gggcgccctcgaagcatgcatctagaggccctattctatagtgctacctaagtctagag 814
Db 11236 GCGGCGCCTCGAGCATCATCTAGAGGCGCCCTATTCTATGTGTCACCTTAATCTGTAG 11177
QY 815 ctgcgtatgaagctgcagctgctcctctagttgcagagcatcgtgtgttgcctccc 874
Db 11176 CTCGCTATGAGCCTTCAGCTGCTGCTTCTAGTTGCGACATCTGTTGTGCCCCCTCC 11117
QY 875 ccgtgcctccttgcaccttggaagtgtgcacactcccatgtccttctctaataaagttag 934
Db 11116 CCGTGCTCTTCATCCCTGGAAGGTGCCAATCCCACTGTGCTTCTTAATAAATGAGG 11057
QY 935 aaattgcatgcattgtcctgaagtagtgcattctatcttcgggggtgtgggtggcgaag 994
Db 11056 AAATTCATGCGCATTTGCTAGTAGTGTGCTATTCTATCTGGGGGGGTGGGGTGGCAGG 10997
QY 995 acaagcaagggggaagatttggaagaacatagcaagcatgctcgtgggaatgctgagccta 1054
Db 10996 ACACGACAGGGGAGAGATTGGGAACAAATAGACAGCATGCTGGGAGATCCGCTGGCTCTA 10937
QY 1055 tggcttctgagcggaagaacacagctgcattaaatgaatcggccaacgcgcggggagag 1114
Db 10936 TGGCTTCTGAGCGCGTA-----TGGGTTGGAATAATACCGCACAGATGCGTAAGGAG 10886
QY 1115 cgtgttcgcatctggtggcgtcttcgcttctcctgcgtacgactcgtgtgcgtgcgt 1174
Db 10885 AAATATACCGATACAGGGGCTTCTCCGCTTCTGCTACGTGACTGCTGGCTGGTCTGT 10826
QY 1175 tcggtcgcgcgagcgtgctacagctcaactcaaaagcgttaacggttaccacaagatc 1234
Db 10825 TCGGCTCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGTTATCCACAGATC 10766
QY 1235 aggggataacgcggaagaacacatgtgagcaaaagcgcagcaaaagccagaacgtaa 1294
Db 10765 AGGGATTAACGACGAGAAACAATGTGAGCAAAAAGGCCACAGCAAAAAGCCAGAAACGTTAA 10706
QY 1295 aaagggcgcgtgctgctgttcttccataggtccgcgcccccgagcagagatatacaaaaa 1354
Db 10705 AAAGGCCGCTGCTGCGGTTTTCATYAGGCTTCGCGCCCTCGACAGCATACAAAAA 10646
QY 1355 tcgacgtcaagtcaagaggtgcgcaaacccgcaagagcatataaagataccaggcgtttcc 1414
Db 10645 TCAGAGCTCAAGTAGAGGTGGGAAAAACCGACAGACGACTATMAAGATACAGAGCGGCTTCC 10586
QY 1415 ccctggaagctccctcgctcctcctgttccgagccctgcggttaccgagatacctgctc 1474


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Db 10585 CCCTGGAAGCTCCCTGCGCTCTCTGTTCCAGACCTGCCGCTTACCGGATACCTGTC 10526
Qy 1475 cgccttcctccctcgggaagcgtgagcgttcctcaatcgaacgtgtagtalcag 1534
Db 10525 CGCCTTCTCCCTTGGGAAGGTGGCGCTTCTCATAGCTCAGCTGAGTATCTCAG 10466
Qy 1535 ttcggtgtagtgcgttcgctcgaagcgtggtgctgctgacgaacccccgtcaccga 1594
Db 10465 TTCGGTGTAGGCTGTCCCTCCAAAGCTGGCGTGTGTGACGAAACCCCGCTCACCCGA 10406
Qy 1595 cgcgcgcctatccggttaactatcgtcttgagtcgaacccggtgaagacacgaacttacc 1654
Db 10405 CGCGTGGCCCTTATCCGTAATCATGCTTGTAGTCCAAACCCGGTAAGACACGACTTATC 10346
Qy 1655 gccactggaacgaacgacctggttaacaggaatagcagaagcgaatgtaggcgtgctac 1714
Db 10345 GCCATGTGACAGCAGCCTGTGTAACAGATTAGCAGACGAGATGTAGGCGGTGCTAC 10286
Qy 1715 agagttcttgaagtggtgcttaactacgctacacgtagaaggaagatattgtgactctg 1774
Db 10285 AGAGTCTTGAAGTGTGGCTTAACCTAGCGCTACACTAGAAAGACAGATTGTGATCTG 10226
Qy 1775 cgcctcgtgaagcagcttaactcgcgaacaaagattgtagctctgacccggaaca 1834
Db 10225 CGCTGTGCTGAAGCCAGTTACTCTTGGAAAAAGACTTGTGACTCTTGTATCCGCAACA 10166
Qy 1835 aaccacgcgtgtagcgtggtttttttgttgcgaagcagaatlaacgcgcgaagaaaa 1894
Db 10165 AACCCACCTCGTACGGTGTGTTTTTTTGTGCAAGCAGCAGATAGCGCGCAGAAAAA 10106
Qy 1895 aggaactaagaagaatccttgatcttctacgaggtctcgaagcgtgtaggaagaaaa 1954
Db 10105 AGGATCTGAAGAAATCCTTGATCTTTCTAGGGGCTGTGAGCTCAGTGAAGCAAAA 10046
Qy 1955 ctcaagttaaaggaatttgatcatagcgaatcacatattgaatgtagga 2007
Db 10045 CTCACGTTAAGGAGATTGTCATGATGATTAATCAAAAAAGATCTTCACCTAGA 9993

RESULT 8
ABA94259/c
ID ABA94259 standard; DNA; 14455 BP.
XX
AC ABA94259;
XX
DT 13-MAR-2002 (first entry)
XX
DE Nucleotide sequence of expression plasmid pE1/Fiber.
XX
KW Adenovirus; Inverter terminal repeat sequence; ITR5; ocular disease;
KW fiber protein; photoreceptor; rhodopsin; starardt disease gene; STDG1;
KW ophthalmological; antiinflammatory; antidiabetic; cytoskeletal;
KW gene therapy; ss.
XX
OS Synthetic.
XX
PN WO200183729-A2.
XX
PD 08-NOV-2001.
XX
PE 30-APR-2001; 2001WO-EP04863.
XX
PR 01-MAY-2000; 2000US-0562934.
XX
PA (NOVS ) NOVARTIS AG.
PA (SCRI ) SCRIPPS RES INST.
PA (NEME/) NEMEROW G R.
PA (VSEG/) VON SEGGERN D J.
PA (FRIE/) FRIEDLANDER M.
PI Nemerow GR, Von Seggern DJ, Friedlander M;
XX
DR WPI: 2002-082846/11.

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XX
PT Polynucleotide for making vectors, useful for treating ocular diseases,
PT e.g., retinitis pigmentosa, comprises adenovirus inverter terminal
PT repeat sequences, packaging signal and photoreceptor-specific promoter
PT
XX
XX Example 1; Page 114-118; 149pp; English.
XX
CC The invention provides an isolated polynucleotide comprising adenovirus
CC (AV) inverter terminal repeat sequences (ITRS), AV packaging signal
CC operatively linked to ITRS and a photoreceptor-specific promoter. A
CC recombinant AV vector (AAV) comprising the polynucleotide is useful for
CC targeted delivery of a gene product to the eye (especially to the
CC vitreous cavity), for treating an ocular disease, e.g., retinal
CC degenerative disease, retinitis pigmentosa, Starardt's disease, diabetic
CC retinopathies, retinal vascularizations, and retinoblastoma, of a mammal
CC preferably human. The AAV comprises a fiber protein that specifically or
CC selectively binds to receptors that are expressed on cells (preferably
CC photoreceptors in the eye). Preferably, the recombinant virus comprise a
CC fiber protein from an adenovirus type B subgroup or is a chimeric protein
CC containing a portion of the N-terminus of an adenovirus type 2 or type 5
CC penton, and the therapeutic product is a trophic factor, an anti-
CC apoptotic factor, gene encoding a rhodopsin protein, a wild-type
CC starardt disease gene (STDG1), an anti-cancer agent and a protein that
CC regulates expression of a photoreceptor specific gene product. The viral
CC nucleic acid of AAV comprises ITRS and packaging signal derived from AAV
CC subgroup B or C, especially an AV type 2 or type 5. AAV is also useful
CC for targeted gene therapy, where the vector comprises an AV type 37 fiber
CC protein or its portion, and selectively transduces photoreceptors and
CC delivers a gene product encoded by AAV. The present sequence represents
CC an expression plasmid pE1/Fiber containing the adenovirus EI and fiber
CC gene.
XX
SQ Sequence 14455 BP; 3698 A; 3271 C; 3565 G; 3921 T; 0 other;
XX
Query Match 14.1%; Score 1148.2; DB 24; Length 14455;
Best Local Similarity 95.5%; Pred. No. 1.6e-162;
Matches 1196; Conservative 0; Mismatches 48; Indels 9; Gaps 1;
Qy 755 ggcgcgcgtcagcatgcatcagtagagggccctattctatagtgtaacaaatgtagag 814
Db 11236 GCGGCCGCTCGAGCATGTCATGAGGCGCCCTATCTATGTCACCTAATATGCTAGAG 11177
Qy 815 ctgcgtatcagcctgcagctgcttcctatagtgccagcaatcgtgtttgcccctcc 874
Db 11176 CTCGCTGATCAGCCCTCGACTGCTGCTTACTAGTGCACACATCTGTTGCCCCCTCC 11117
Qy 875 ccgtgccttccttgcacctggaagtgccactcccaatgcttcctcaataaataagag 934
Db 11116 CCGTGCCTTCTTGACCTCGGAAGGTGCACCTCCACTGTCCTTCTTAATAAATGAGG 11057
Qy 935 aaatgcacatgctcgtgtagtgatgtcatctatctctggtgggtggtggtggtggtg 994
Db 11056 AAATGCATCCGATTTGTGTAGTAGTGTCTATCTATCTGCGGGGTGGGTGGGCAAG 10997
Qy 995 acaagcaagggggaagattgggaagacaatagcaagcagtcgtggtggtggtggtggtg 1054
Db 10996 ACAGCAAGGGGAGGATTTGGGAAGCAATAGCAGGATGTGGGATCGGTGGCTCTTA 10937
Qy 1055 tgccttcgtaggctggaagaacacagctgcatatgaatcggtcccaacgcgtgggtggtg 1114
Db 10936 TGGCTTCTGAGGCGGTA-----TCCGGTGTGTAATACCGCACATCGTAAAGAG 10886
Qy 1115 cgtttggtatattggggcgtcttcgccttcgtcgttaactgaactgcgtgcgtgctgct 1174
Db 10885 AAATACCGCATCAGGCCCTCTTCGCTTCTCGTCACTGATCGCTGCGCTCGGTGCT 10826
Qy 1175 tcgcttcgagcagcagtgatcactcaaaagcgtgtaataagttatcaagaatc 1234
Db 10825 TCGGCTGGGGAGGAGGTATCAGCTCACTCAAGCGGTGTATATAGGTTATCACAGATTC 10766
Qy 1235 aggggatacgcgaagaaacatgtgagcaaaagggccagcaaaagccaggaacgttaa 1294

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Accession	Gene	Position	Sequence	Length
Db 10765	AGGATATACCGACGAAAGAACATGTGACCAAAAGGCCAAGAGCCAGGAACCTGTAA	10706		
Oy 1295	aaaggccgcgctgtctgtgcgttttccataaggctccgccccctgacgagcatcacaanaa	1354		
Db 10705	AAAGCCCGCGTGTGCTGGCGGTTTTTTCATTAAGGCTCCGCCCCCTGACGAGCATACAAAAA	10646		
Oy 1355	tcgaagcctcaagtcagaaggttgcgaaccgcagagactaaagaatccagcggttcc	1414		
Db 10645	TCGAGCGTCAAGTCAAGAGGTGGCGGAACCCACAGAGCACTATTAATAATACAGGGCTTTTCC	10586		
Oy 1415	cccttgaagctcccttcgcgtcctccctgttccgagcctgcgcgtcttaccgatactgtc	1474		
Db 10585	CCCTGGAAAGCTCCCTCGTGGCGGTCTCGTTCGACGACCTGGCGGCTTACCGGATACCTGTCC	10526		
Oy 1475	cgctcttcccttcgcgggaagcgttgcgcttctcgaatgtcgaegctgtlaagatctag	1534		
Db 10525	CGCCCTTCTCCCTTCGGGAAGGTGGCCCTTCTCATAGCTACAGCTGTAGTATCTCAG	10466		
Oy 1535	ttcgtgtgaagtcgtctgcgtcccaagcttgcgtctgtgtgaagaaacccccgttcaacccga	1594		
Db 10465	TTCCGGTGAAGTCTGTTCTCTCCACAGCTGGGCTGTGTGACAGAACCCCGTTCAACCCGA	10406		
Oy 1595	ccgctgcgccttaccggtlaactatcgtctgtagtgtccaaaccgcgtgaagacacgaactatc	1654		
Db 10405	CCGGTGCCTTTATCCGGTAACCTATCGTCTGAGTCCAAACCGGTAAACACAGCACTTATTC	10346		
Oy 1655	ggccctggaagcagcagcacttgttaacagatattagcagaagcagaagtattgtagcgtgtctac	1714		
Db 10345	GCCACTGGCAGCAGCCACTGTGTATACAGGATTAAGCAGACGAGGTATGTAGGCGGTCTAC	10286		
Oy 1715	agagctcttgaagttgtgtgccttaactacggtctacactagaagagacagatattgtatctg	1774		
Db 10285	AGAGTCTTTGAAGTGTGTGGCTCACTACGGCTACACTGAAGAGACAGTATTTGGTATCTG	10226		
Oy 1775	cgctctgtctgaagcaggttacccttcgagaaagaagtgtgtgctctgtatccgcgacaaca	1834		
Db 10225	CGCTCTGCTGAAGCCACTGTGTACCGGAAAAAGATTGTGTGCTTGTATCCGGCAAAACA	10166		
Oy 1835	aaccacgcgtgtagcgttgttcttctgtctgaagcagcagattacgcgcagaaaaa	1894		
Db 10165	AACCAACGCTGTAGCGGTGTGTTTTTGTTCGACAGCAGCAGATTACGCCAGAAAAA	10106		
Oy 1885	aggatctcaagaagaatccttgcattcttctcaagggctcgtgacgctcagtgcgaacgaaa	1954		
Db 10105	AGGATCTCAAAAGATCTTGTGATCTTTTTCACGGGGCTGTACGGCTCAGTGGAAAGAAAA	10046		
Oy 1955	ctcacgttgaaggaatttgcgtcatgagaggtacattgaatgatattaga 2007			
Db 10045	CTCACGTTAAAGGATTTTGGTCATGAGATTATCAAAAAAGATCTTCACTTAGA 9993			
RESULT 9				
AC	AAA53872			
XX	AAA53872 standard; DNA; 5377 BP.			
XX	AAA53872;			
XX	03-JAN-2001 (first entry)			
XX	Expression vector pRIG14.			
DE	Vector: endogenous gene; activation; over-expression;			
KW	erythropoietin; growth hormone; drug discovery;			
KM	granulocyte colony stimulating factor; ds.			
KW	Synthetic.			
OS				
XX	WO200049162-A2.			
PN				
PD	24-AUG-2000.			
XX				
XX	22-FEB-2000; 2000WO-US04429.			
XX				
XX				
XX				

[illegible]

QY	503	tttggacccaataatcaacgggacttcccaaaatgtctgtacacact-----ccggcccc	554
Dp	2537	ttctggcccccaaaacaacgggactctcccaaaatgtctgtacaacactgcgactcgccggcccc	25966
QY	555	atttcagccaatatgggcgtgtagcgtgtgtacggctggagagcttatataagcagaagctctctg	614
Dp	2597	gttgcagccaatatgggcgtgtagcgtgtgtacggcgtgtatatataagcagaagctctctt	26566
QY	615	gctactaagagaacccaact-----gcttactgtgcttacc	648
Dp	2657	agttgaaccggtctcagatccactctcgaagttaattctgcgttgaattatcaacagtttaaatgtgtacac	27166
QY	649	gaattatatacgaatactactatagggagaccgaacgtctgtgtacagagctcgcgatccacag	708
Dp	2717	gcaactcagctgtctctctgtgacaacaacagctctcgaacttaagctgcagtgactctcttaattaa	27766
QY	709	taacggcccgccagctgtg-----	725
Dp	2777	ccacacgctatacagtgtagtactcgtatcgtactctacctaagaagggcgtctatctgtgccagta	28366
QY	726	-----	725
Dp	2837	gcagtcgaagaagaagaagtttaagagagccggaacaaagcgtctcatatgagcccggaagctgycga	28966
QY	726	-----cttggaaattctgtcagaatatctccatcacactgtgcgccc	760
Dp	2897	gcccgactctcccatctcgtgtagctgtcgtgagatataagtcgcgcgaagcaacgcgaactgtgtgcg	29566
QY	761	gctcgcagcatcgtacatctagagagccctactctatagtgtaacttaatgctcgaagctcgc-	819
Dp	2957	ccggctgtagtcgcggccacagatgctgtccggcggtatagagagatccacaagagcgggtgtgtgtctgc	30166
QY	820	---tgacacagccctcgcagactgtgtgcctctctagtctgcgaagccactgtgtgttggccccccccc	876
Dp	3017	atgactcgcgtctagctcgtacatagctgtctccaagttagcgaagcgaagcactcgtggcgcgcgcga	30766
QY	877	gtgcctctccttga-----	889
Dp	3077	aagcgctcgcgaacagtgctcccggaagaaggtgtgcgtatagaataattgcatcaacgatalatagc	31366
QY	890	-----cccttggaaaggtgtgccaactcccatctccattctcta	923
Dp	3137	gctcgtactccttctagagctcgcgaagcccgacacggctggtagagctccagacttctgttctccct	31966
QY	924	ataaataatgagaagaattgtcattcgcgatctgtctgcgtataggtgtctatctctatctctgggg	978
Dp	3197	tagtgaaggtgttaattctcgaagcttgcgttaatacattgctacatagctgttctcgtgtgttgaaa	32566
QY	979	-----gttgggggtgtgggcagggacagggcaagggggaggg	1009
Dp	3257	ttgttatccgctcaacaattccacaacatacgcgcgggaagcattaagaagtataagctctgg	33166
QY	1010	atttggagagacaataagcagagcagctcgtggagatgcgggtgtggctctatctgtctct-----	10626
Dp	3317	gtgcctaattagtgtaggttaactcatcatlaattatgtgtgtgtgcctcactgcgcgcctcttcag	33766
QY	1063	---gagcggaagaagaacacagctctgtcatatataatgcgcgaacgcgcggggagagcggtt	1119
Dp	3377	cgggaaaaacctgtcgtgtgcacagctgtgcattatgtaatcctgcgaacgcgcggggagagcggtt	34366
QY	1120	tgcgtatcttggcgctctctccgcgtctctctctgcgtcaactaacccgtctgcgtctgcgttctgc	1179
Dp	3437	tgcgtatcttggcgctctctccgcgtctctctctgcgtcaactaacccgtctgcgtctgcgttctgc	34866
QY	1180	tgcgcgcagcgcgttatcagctcactcacaagcggttaatacgtgttatccacagaatatcgggg	1239
Dp	3497	tgcgcgcagcgcgttatcagctcactcacaagcggttaatacgtgttatccacagaatatcgggg	35566
QY	1240	ataacgcagagaagaagaacatgtgtgcgaagaagcgcaagaagaagccggtataaagg	1299
Dp	3557	ataacgcagagaagaagaacatgtgtgcgaagaagcgcaagaagaagccggtataaagg	36166
QY	1300	ccggcgttgcctggcgctttttccataagctctccgcgcctccctgtacgagcatatacaaaaatccac	1359

Db	3617	ccgcgcttcgcggtcttttccataagctccgcgcctcccttcgacgagcaatccaaataatcgac	3676
Qy	1360	gtctaaagctcagaggttggcgaatacccgacagagactataaagatacaagcgctttcccttg	1419
Db	3677	gtctaaagctcagaggttggcgaatacccgacagagactataaagatacaagcgctttcccttg	3736
Qy	1420	gaagctccctccgctgcgtctctctgttcgcgaacctgcgcgtcttacccggaatactgtccgct	1479
Db	3737	gaagctccctccgctgcgtctctctgttcgcgaacctgcgcgtcttacccggaatactgtccgct	3796
Qy	1480	ttccctccctcggaagacgttgcgtcttctccaaatgtctcaacgctgtatggatctcagtcgg	1539
Db	3797	ttccctccctcggaagacgttgcgtcttctccaaatgtctcaacgctgtatggatctcagtcgg	3856
Qy	1540	ttgatgtcgttcgctccaaagcttggcgctgtgtcgaacgaaccccccgttcagccgacgcgt	1599
Db	3857	ttgatgtcgttcgctccaaagcttggcgctgtgtcgaacgaaccccccgttcagccgacgcgt	3916
Qy	1600	ggcgcttatccggttaactatcgtcttgagttccaaacccggttaagacagacattatccgcac	1659
Db	3917	ggcgcttatccggttaactatcgtcttgagttccaaacccggttaagacagacattatccgcac	3976
Qy	1660	ttggcagcagccacattgttaacagagattagacagacgaggttatgtagcgggtgtctacaagt	1719
Db	3977	ttggcagcagccacattgttaacagagattagacagacgaggttatgtagcgggtgtctacaagt	4036
Qy	1720	ttcttgaagttgttgctctaactaacggtctacatacagaagaacagatttgtatctgcgctc	1779
Db	4037	ttcttgaagttgttgctctaactaacggtctacatacagaagaacagatttgtatctgcgctc	4096
Qy	1780	ttgtcgaagccaattaccttcggaanaaagatttggtagctccttgcataccgcgcaacaaccca	1839
Db	4097	ttgtcgaagccaattaccttcggaanaaagatttggtagctccttgcataccgcgcaacaaccca	4156
Qy	1840	ccgcgttgcgtacggttggttttttgtttgttcgaagcagcagattacgcgcgcaaaaaaggat	1899
Db	4157	ccgcgttgcgtacggttggttttttgtttgttcgaagcagcagattacgcgcgcaaaaaaggat	4216
Qy	1900	ctcaagaagaagtccttgaatcttttctacaggggtctgcagcctcaagtcggaacaaactcac	1959
Db	4217	ctcaagaagaagtccttgaatcttttctacaggggtctgcagcctcaagtcggaacaaactcac	4276
Qy	1960	gttaaggatatttgcatactagcgcgaatacatatttgaatgatacttaga	2007
Db	4277	gttaaggatatttgcatactagcgcgaatacatatttgaatgatacttaga	4324
RESULT 10			
AAAS3870 standard; DNA; 4645 BP.			
XX	1D	AAAS3870 standard; DNA; 4645 BP.	
XX	AA		
XX	AC	AAAS3870;	
XX	DF	03-JAN-2001 (first entry)	
XX	DE	Expression vector pRIG21b.	
XX	XX		
KW	Vector; endogenous gene; activation; over-expression;		
KW	erythropoietin; growth hormone; drug discovery;		
KW	granulocyte colony stimulating factor; ds.		
XX	OS	Synthetic.	
XX	PN	W0200049162-A2.	
XX	PD	24-AUG-2000.	
XX	PF	22-FEB-2000; 2000MO-US04429.	
XX	PR	19-FEB-1999; 99US-0253022.	
XX	PR	08-MAR-1999; 99US-0263814.	
XX	PR	26-MAR-1999; 99US-0276820.	


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Db      852  tcttaataccacacatggtctacaggtgagtgactcgtctacctaagaagagcgctatctggcc  911
Qy      794  aggttcacccaataatgctacaggtcgcgtgacacagctcgtactggtccttaagtgtccagc  853
Db      912  agttaagcagctcgaagaagaagtttaagaagacgcgaacaacagcgtcatatgagcccgag  971
Qy      854  catctgtgtgttgcacctcccccgttccttccttgacccttggaagtgccacatcccaatg  913
Db      972  ggcgaagccgcatcttcccccctcgtgtatgtcgcgcgatatatagcgccagcaacgcgacctg  1031
Qy      914  tcccttccctaataaatatgagaatgtcatgcgactgtctgagtaagtgtcatctatc  973
Db      1032  t-----  1032
Qy      974  ttgggggtgtgggtgtgggagcaagacagcagggaggaatgttggaagacaatagcagcgatg  1033
Db      1033  ----gagcccggtgattgcggccacagatgcgtccgcgtagagatccacagagcgggtg  1088
Qy      1034  ctggggatgcgggtgggtctctatgtctctcgtgagcggaagaacacagctgcatatgaat  1093
Db      1089  tggtcgccatgat-----cgcgtagtcgatagtg  1117
Qy      1094  cggccaaacgcgcgggagagagcggttgcgtatgtggcgctcttcgcgtccctcgcgtcac  1153
Db      1118  gcccaaatagtcgaagcagcagcagactggtgcgcgcgccaagcggtcgcgaagtgctcccg  1177
Qy      1154  tgcactgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1213
Db      1178  agaacgggtgcgcatagaaattgcatcaaatatagcgtatagctctgtcgtcgtcgtcgtcgt  1237
Qy      1214  aatacgttataccacagaatcagggtataacgcgaagaagaacatgtgaaacaaaggcca  1273
Db      1238  agatcgtcgaag-----catggaacaaaggcca  1268
Qy      1274  gcaaaagccaggaacccgtataaaagcgcggttgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1333
Db      1269  gcaaaagccaggaacccgtataaaagcgcggttgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1328
Qy      1334  cctctgcagacatcaacaaataatcgaagcgtcaaatcagaagttggtgcgaacccgcgaagact  1393
Db      1329  cctctgcagacatcaacaaataatcgaagcgtcaaatcagaagttggtgcgaacccgcgaagact  1388
Qy      1394  ataagaatacagagcggttcccccctggaagctccctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1453
Db      1389  ataagaatacagagcggttcccccctggaagctccctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1448
Qy      1454  gccgcttacgcgaatacctgtcgcgtccttcccttcgcgggaagcgtgtgcgtcttcctcaatg  1513
Db      1449  gccgcttacgcgaatacctgtcgcgtccttcccttcgcgggaagcgtgtgcgtcttcctcaatg  1508
Qy      1514  ctacgctgtgaggtatctatcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt  1573
Db      1509  ctacgctgtgaggtatctatcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt  1568
Qy      1574  cgaaccccccttcagccccacacgcgtgcgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1633
Db      1569  cgaaccccccttcagccccacacgcgtgcgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1627
Qy      1634  cccggttaagaacacgactatcgcgaactgtgcagcagcgaactgtgtaacagatagcagagc  1693
Db      1628  cccggttaagaacacgactatcgcgaactgtgcagcagcgaactgtgtaacagatagcagagc  1687
Qy      1694  gaaggtatgtagcgtgtcgtacagagttcttgaagttgttgccctaactagcgtacacctag  1753
Db      1688  ga-gtatgttagcgtgtcgtacagagttcttgaagttgttgccctaactagcgtacacctag  1746
Qy      1754  aaggacagtaattgttatctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1813
Db      1747  aaggacacataattgttatctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt  1806
Qy      1814  tagctcttgatccgcgaacaaacacgcgtgtgtaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt  1873

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```

Db      1807  tagctcttgatccgcgaacaaacacgcgtgtgtaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt  1866
Qy      1874  gcagattacgcgcgaagaaaaaagatcctaagaagatcctttgattctttttcttcagggtc  1933
Db      1867  gcagattacgcgcgaagaaaaaagatcctaagaagatcctttgattctttcttcagggtc  1926
Qy      1934  tgaacgtcaatgtggaacgaacacacgttaaggatttggatcatagcgcgaatacatt  1993
Db      1927  tgaacgtcaatgtggaacgaacacacgttaaggatttggatcatagcgcgaatacatt  1986
Qy      1994  tgaatgbattaga 2007
Db      1987  gatcttcacctaga 2000

RESULT 14
AAV40007
ID      AAV40007 standard; DNA: 4026 BP.
XX
XX
AC      AAV40007;
XX
DT      15-FEB-1999 (first entry)
XX
DE      Plasmid pCTMI.
XX
KW      E2F: transcription factor; human; retinoblastoma protein RB;
KW      bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW      thyroid hyperplasia; Grave's disease; psoriasis;
KW      benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW      peripheral vascular disease; therapy; plasmid pCTMI; ss.
XX
OS      Chimeric - cytomegalovirus.
OS      Chimeric - mastadenovirus.
OS      Chimeric - bacteriophage T7.
OS      Chimeric - bacteriophage SP6.
OS      Chimeric - rhesus macaque polyoma virus.
OS      Chimeric - Bos taurus.
XX
FH      Key
FT      promoter
FT      misc_feature
FT      intron
FT      misc_feature
FT      promoter
FT      intron
FT      misc_feature
FT      CDS
FT      W09021228-A1.
FT      22-MAY-1998.
FT      13-NOV-1997; 97WO-US21821.
FT      14-FEB-1997; 97US-0801092.
FT      15-NOV-1996; 96US-0751517.
FT      (CANF-) CANJ1 INC.
FT      Antelman D, Gregory RJ, Willis KN.
FT      WPI; 1998-297858/26.
XX

```


PT New fusion polypeptide of, e.g. transcription factor - used to
PT treat, e.g. hyper-proliferative disease such as cancer and
PT restenosis

XX Example 1; Fig 6; 91pp; English.

XX This is the nucleotide sequence of pCTM1, a plasmid that was
CC constructed from pCTM (see AAV4006) by digesting pCTM with XhoI and
CC NotI and subcloning a 180 bp intron XhoI-NotI fragment from a
CC PCMV-beta-gal vector. Plasmid pCTM1 has been used as a vector for
CC the expression of fusion proteins of the invention that comprise
CC retinoblastoma protein (BP, see AAW62465) and E2F transcription
CC factor (see AAW62464). Such fusion proteins, particularly expressed
CC from gene therapy vectors, are used to treat hyperproliferative
CC conditions, specifically cancer (particularly of the bladder) or
CC restenosis. They are more effective in repressing transcription of
CC the E2F promoter than RB alone and cause cell-cycle arrest in a
CC variety of cells.

XX Sequence 4026 BP; 978 A; 1021 C; 982 G; 1045 T; 0 other;

Query Match 13.2%; Score 1070.2; DB 19; Length 4026;

Best Local Similarity 69.7%; Pred. No. 7.4e-151;
Matches 1919; Conservative 0; Mismatches 88; Indels 746; Gaps 5;

QY 1 gatgtacggccagatatacagctgtgacatgtatattgactagttatataagtaacaa 60
Db gatgtacggccagatatacagctgtgacatgtatattgactagttatataagtaacaa 269
QY 61 attacgggttattatgattacatagcccatatgtgagttccggttactaactaagta 120
Db attacgggttattatgattacatagcccatatgtgagttccggttactaactaagta 329
QY 121 aatgagccgctgtgctgacccgccaagaccccccgcattgagctacataatgacgtat 180
Db aatgagccgctgtgctgacccgccaagaccccccgcattgagctacataatgacgtat 389
QY 181 gtcccatagtaacgcaaataggaacttccattgacgtacaaatgggtgacattatcag 240
Db gtcccatagtaacgcaaataggaacttccattgacgtacaaatgggtgacattatcag 449
QY 241 taactgcccacttggcagctatcatatgaatgtatcatatgccaagtacgccccatttac 300
Db taactgcccacttggcagctatcatatgaatgtatcatatgccaagtacgccccatttac 509
QY 301 gtcaatgacgtaaatggccgctgcatatgcccagtaacatgactttgagacttt 360
Db gtcaatgacgtaaatggccgctgcatatgcccagtaacatgactttgagacttt 569
QY 361 cctacttggcagctatcatatgacttgcgtatcgtatcattaccatggtatgctgtttg 420
Db cctacttggcagctatcatatgacttgcgtatcgtatcattaccatggtatgctgtttg 629
QY 421 cagtaacatcatggcggtgatatgaggttttactacgaggatcccaagctccacccc 480
Db cagtaacatcatggcggtgatatgaggttttactacgaggatcccaagctccacccc 689
QY 481 attgacgtcaatggaggtttgttttggcacaacaatacagggactttccaagaatgctgt 540
Db attgacgtcaatggaggtttgttttggcacaacaatacagggactttccaagaatgctgt 749
QY 541 aacaactcggcccatatgacgcaaatggcggttagcggtgtaacggttggaagtctata 600
Db aacaactcggcccatatgacgcaaatggcggttagcggtgtaacggttggaagtctata 809
QY 601 agcagagctctctgtgctactaagaaacccactgtctactgtgtaatcgaataatcag 660
Db agcagagctctctgtgctactaagaaacccactgtctactgtgtaatcgaataatcag 869
QY 661 actcaactaagagacccaagcttgg----- 687
Db actcaactaagagacccaagcttggcgcggtgtacacactctcttcgcgacgcgtctgt 929

QY 688 ----- 687
Db cgaggcgacgtgtgtggtctgcggttgtaggaaacactcttcggtcttccagtaactc 989
QY 688 ----- 687
Db ttgagtcgaaacccgctgcggtctccgaaacgtaactccgcaacgagagactgagcagt 1049
QY 688 ----- 687
Db ccgcatgcacggtatcggaacactctcgcaggaactcaaaaaccagaagaattacgtgta 1109
QY 688 ----- 723
Db agttagcttttgccttttatttcaagtcggtccggtacggtgtgtgtaacataaag 1169
QY 724 tgcgtgaattctgagatat----- 743
Db aactgctcctcagtggaagtgcttactctcagcctgtaaggaagtgttactctgc 1229
QY 744 ----- 774
Db tctaaagctgcggaattgtacccgcgctgacgtcagttacagaaatcgcgtacgata 1289
QY 775 ctgaaggccctattctatagtgtaacacaaatgctgagctgcgtatcagctgcgact 834
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QY 835 gtgcctctatgttcgcagcaactgctgtgttggcccccgcgctccttccttgcacctg 894
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QY 895 gaaggtgccaactccacgtctccttctcctaataaataaggaatgtgacatgctgtctg 954
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QY 955 agtagtgtaacttctatctctggtggtgtggttggcgacgacgaagggtggaagtgtg 1014
Db agtagtgtaacttctatctctggtggtgtggttggcgacgacgaagggtggaagtgtg 1529
QY 1015 gaagaaatagcagatcgtcgtggga----- 1040
Db gaagaaatagcagatcgtcgtggga----- 1040
QY 1041 ----- 1040
Db ttccacgcgcgcttctatgaaggttggtcgtcgaatcgttttcgggagcgcgctg 1649
QY 1041 ----- 1040
Db gatgatcctccagcgcggtgatactcatgctggaattcttcgcccacccaactgtttat 1709
QY 1041 ----- 1040
Db tgcagctatataatggttaacaataaagcaatagcatcaacaattccacaataaagcatt 1769
QY 1041 ----- 1040
Db ttttcaactgtatctggtgtgtgttgcacaactcaatcaatgtaattatcatgtctgt 1829
QY 1041 ----- 1040
Db tatacgcgcacccctagtagagcttgcgtlaatcatgtaacatgctgttctgtgtg 1889
QY 1041 ----- 1040
Db aaattgtatcgcgtcacaattccacaacaacatcagcgccggaagcatabaagtgttaagc 1949
QY 1041 ----- 1062
Db ctgggtgtcctaaatgagtgagctaacctcaactaattatggtgttgcgtccacacgcgcgttt 2009

OY	1063	-----ggggcggaagaagacaagctctgataatgaatcggccaagccgcggggagag	1114
Db	2010	ccagctcggaagaaacccctctgtccagagctgataatgaatcggccaagccgcggggagag	2069
OY	1115	cggtctcgatctggagcgctctccgctccctccgcacatctgactgcgcgtcgtcgt	1174
Db	2070	cggttctcgatctggagcgctctccgctccctccgcacatctgactgcgcgtcgtcgt	2129
OY	1175	tcggctcgcgagagcggtatcaagctcaactcaagaagcggtgaatacgttatccacagaatc	1234
Db	2130	tcggctcgcgagagcggtatcaagctcaactcaagaagcggtgaatacgttatccacagaatc	2189
OY	1235	aggggatataagcagcggaaagaacatctggaacaaaggccagacaaaggccaggaacggtaa	1284
Db	2190	aggggatataagcagcggaaagaacatctggaacaaaggccagacaaaggccaggaacggtaa	2249
OY	1295	aaagagccgcgtctgactgcgtctttctccataggtctccgcccccttgacagagctcaaaaa	1354
Db	2250	aaagagccgcgtctgactgcgtctttctccataggtctccgcccccttgacagagctcaaaaa	2309
OY	1355	tcgagcgtcaagtccagagtgctgagcgaaaacccgacagagactataagaataccagcgcttcc	1414
Db	2310	tcgagcgtctcaagtccagagtgctgagcgaaaacccgacagagactataagaataccagcgcttcc	2369
OY	1415	cccggaagactccctcgtgcgtctctcgtcttcgcgaacctgcgcgtctacaggaatacgtctc	1474
Db	2370	cccggaagactccctcgtgcgtctctcgtcttcgcgaacctgcgcgtctacaggaatacgtctc	2429
OY	1475	cgctctctcccttcgggaagcgttgcgctctctccaatgctcacgctgtaagatctcag	1534
Db	2430	cgctctctctcccttcgggaagcgttgcgctctctccaatgctcacgctgtaagatctcag	2489
OY	1535	ctcggtgtaagtgctgtccgcacaaagctctggcggtgtgtgcacggaaccccggtctgagccga	1594
Db	2490	ctcggtgtaagtgctgtccgcacaaagctctggcggtgtgtgtgcacggaaccccggtctcagccga	2549
OY	1595	ccgctgcgcctatccggtlaactatcgtctctgagtccaaccccggtgaagacacgaattatc	1654
Db	2550	ccgctgcgcctatccggtlaactatcgtctctgagtccaaccccggtgaagacacgaattatc	2609
OY	1655	ggccactgagcagcagcgaactctgttaacagagatttagcagagcgagtatctgtgagcggtgtcac	1714
Db	2610	ggccactgagcagcagcgaactctgttaacagagatttagcagagcgagtatctgtgagcggtgtcac	2669
OY	1715	agagatctctgaagtgtgtgacctactacacgctctacactagaagaacagatcttgatctg	1774
Db	2670	agagatctctgaagtgtgtgacctactacacgctctacactagaagaacagatcttgatctg	2729
OY	1775	cgctctctgtaagcgaattacctcttcgaaaaaggtctgtagctctctgtatccgcgcaaca	1834
Db	2730	cgctctctgtaagcgaattacctcttcgaaaaaggtctgtgtagctctctgtatccgcgcaaca	2789
OY	1835	aaacacgcgcgtgtagcgtgtcttcttcttgcaagcagcagatcttaacgcagaaaaaa	1894
Db	2790	aaacacgcgcgtgtagcgtgtcttcttcttgcaagcagcagatcttaacgcagaaaaaa	2849
OY	1895	agagatctcaagaagatcctcttgatctcttctctacacgggtctgtacgctctgtagaagcaaaa	1954
Db	2850	agagatctcaagaagatcctcttgatctcttctctacacgggtctgtacgctctgtagaagcaaaa	2909
OY	1995	ctcagcgttaaggagatttctgtaatgtagcgagatacatattgaatgtatttga 2007	
Db	2910	ctcagcgttaaggagatttctgtaatgtagagatctacaaaagaacatctcacctaga 2962	
RESULT	15		
XX	AAZ23778		
XX	AAZ23778 standard: DNA: 8705 BP.		
XX	AAZ23778:		
XX	14-JAN-2000 (first entry)		

DE	Vector pShuttle DNA.
XX	
RW	Antisense; DNA library; identification; multiple cloning site; MCS;
KW	inhibition; ss.
XX	
OS	Synthetic.
XX	
PN	WO9950457-A1.
XX	
PD	07-OCT-1999.
XX	
PE	28-MAR-1999; 99WO-US06742.
XX	
PR	28-MAR-1998; 98US-0079792.
XX	
PR	06-NOV-1998; 98US-0107504.
XX	
PA	(UTAH) UNIV UTAH RES FOUND.
XX	
PI	Ruffner DE, Pierce ML, Chen Z;
XX	
DR	WPI; 1999-610866/52.
XX	
PT	Production of antisense libraries, used for identifying antisense
XX	agents and for identifying target sites for antisense-mediated
PT	inhibition of a selected gene -
XX	
ES	Claim 16; Page 43-50; 63pp; English.
XX	
CC	This invention describes a novel method for generating an antisense
XX	library targeted to a selected RNA transcript. The methods can be used
CC	for identifying antisense agents and for identifying target sites for
CC	antisense-mediated inhibition of a selected gene. The use of a direct
CC	library for target site selection significantly simplifies the screening
CC	process, since only very small libraries need be prepared and assayed.
CC	This sequence represents the vector pShuttle which is used in the method
CC	of the invention.
XX	
SQ	Sequence 8705 BP; 1875 A; 2575 C; 2078 G; 2177 T; 0 other:
XX	
Query Match	13.2%; Score 1068; DB 20; Length 8705;
Best Local Similarity	99.9%; Pred. No. 1.4e-150;
Matches 1079; Conservative	0; Mismatches 0; Indels 1; Gaps 1.
OY	1 gatgacggcgccagatatacgaacgcgttgacattgatattgactagttaataagaatca 60
Dd	2708 gatgacggcgccagatatacgaacgcgttgacattgatattgactagttaataagaatca 2767
OY	61 attacggggtcaatgaattcatatagcccataatgsgttccgcgttacaataactaacgta 120
Dd	2768 attacggggtcaatgaattcatatagcccataatgsgttccgcgttacaataactaacgta 2827
OY	121 aatggccgcgcctggttagccgcgaacgaccgccgccttcgaactlcaataatgaagtat 180
Dd	2828 aatggccgcgcctggttagccgcgaacgaccgccgccttcgaactlcaataatgaagtat 2887
OY	181 gtcccatagtaacgcccataaggagacttccaattgacgtlcaaattgggtgacctataacg 240
Dd	2888 gtcccatagtaacgcccataaggagacttccaattgacgtlcaaattgggtgacctataacg 2947
OY	241 taactgtccccacttggcaggtatatcaaatgtatataatgaccaagtaagccccctattgac 300
Dd	2948 taactgtccccacttggcaggtatatcaaatgtatataatgaccaagtaagccccctattgac 3007
OY	301 gtccaatgcggtaaattgcccgcgcctgcgcatatgcccagtaacatgacctatggagactt 360
Dd	3008 gtccaatgcggtaaattgcccgcgcctgcgcatatgcccagtaacatgacctatggagactt 3067
OY	361 cctactggcaggtacatcttaacgtattatgcatcgcgtctattaccatggttgtgcggtttgg 420
Dd	3068 cctactggcaggtacatcttaacgtattatgcatcgcgtctattaccatggttgtgcggtttgg 3127
OY	421 cagtagcctaataatgagcctgataagcaggttttgaacttacagaggaatttcgaatgtccacccc 480

```
Db 3128 cagtaacatcaatggcgctggaatagcgtcttgaccacaggagattccaaagctccacccc 3187
QY 481 atgacgtcaatggagtttcttggcacaacaatcaacggagacttccaaaatgtcgt 540
Db 3188 atgacgtcaatggagtttcttggcacaacaatcaacggagacttccaaaatgtcgt 3247
QY 541 aacaactccgcccattgaagcaaatggggcgttagcggtgacgttgagggtctatata 600
Db 3248 aacaactccgcccattgaagcaaatggggcgttagcggtgacgttgagggtctatata 3307
QY 601 agcagaactctcttgacctaagagaaccactgctt-actggcttatcgaaattaatatc 659
Db 3308 agcagaactctcttgacctaagagaaccactgctt-actggcttatcgaaattaatatc 3367
QY 660 gactcaactataggaggacccaagcttggtaacgagctcgatccactagtaacgagcgcc 719
Db 3368 gactcaactataggaggacccaagcttggtaacgagctcgatccactagtaacgagcgcc 3427
QY 720 agtgtgtggaattctgcagatatccatcacactggcgccgctcgagcatgcatctaga 779
Db 3428 agtgtgtggaattctgcagatatccatcacactggcgccgctcgagcatgcatctaga 3487
QY 780 ggagccatattctataggtgtacccctaataatgctaagagctcgatcagctgactgtgcc 839
Db 3488 ggagccatattctataggtgtacccctaataatgctaagagctcgatcagctgactgtgcc 3547
QY 840 ttctagtgcagacatctgtgtttgcccctcccccgtgaccttcccttgacccttgaaag 899
Db 3548 ttctagtgcagacatctgtgtttgcccctcccccgtgaccttcccttgacccttgaaag 3607
QY 900 tggcaactcccaactgtctcttccataataatgaggaatgtcatcgcatgtctgagtag 959
Db 3608 tggcaactcccaactgtctcttccataataatgaggaatgtcatcgcatgtctgagtag 3667
QY 960 gtgtcatctatctctggggggtgggggtgggcaagacagcaagggggagagattgggaaga 1019
Db 3668 gtgtcatctatctctggggggtgggggtgggcaagacagcaagggggagagattgggaaga 3727
QY 1020 caatagcagagcatgtctggggaatgcggtgggtctctatggtctctgagcggaagaaccag 1079
Db 3728 caatagcagagcatgtctggggaatgcggtgggtctctatggtctctgagcggaagaaccag 3787
```

Search completed: May 24, 2002, 03:46:09
Job time: 13566 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 00:30:03 ; Search time 134.6 Seconds
(without alignments)
14809.182 Million cell updates/sec

Title: US-09-778-516A-1

Perfect score: 8115
Sequence: 1 gatgtacggcgacagatatcac.....gcgtctgcctagcagcagtc 8115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/prodata/2/lna/5A.COMB.seq:*
- 2: /cgn2_6/prodata/2/lna/5B.COMB.seq:*
- 3: /cgn2_6/prodata/2/lna/6A.COMB.seq:*
- 4: /cgn2_6/prodata/2/lna/6B.COMB.seq:*
- 5: /cgn2_6/prodata/2/lna/PCITUS.COMB.seq:*
- 6: /cgn2_6/prodata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1240.4	15.3	3853	3	US-08-801-092-5
2	1068.6	13.2	4026	3	US-08-801-092-19
3	1053.6	13.0	4326	4	US-08-760-615-7
4	981.8	12.1	6253	3	US-08-893-327-15
5	981.8	12.1	6280	3	US-08-893-327-17
6	981.8	12.1	6280	3	US-08-893-327-19
7	973	12.0	4283	1	US-08-343-403A-3
8	973	12.0	4283	1	US-08-445-265A-1
9	973	12.0	4283	3	US-08-990-442-1
10	968.2	11.9	3987	4	US-09-082-649B-83
11	961.8	11.9	3987	4	US-09-082-649B-84
12	921.8	11.4	6285	1	US-08-467-420A-49
13	921.8	11.4	6285	1	US-08-470-110A-48
14	921.8	11.4	6285	1	US-08-667-769A-49
15	921.8	11.4	6285	2	US-08-940-371-49
16	921.8	11.4	6285	2	US-08-637-647-49
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25	906.4	11.2	4540	1	US-08-770-761A-6
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30	906.4	11.2	4883	1	US-08-064-121-4	Sequence 4, Appl
31	906.4	11.2	4883	1	US-08-318-172A-1	Sequence 1, Appl
32	906.4	11.2	4883	1	US-08-478-015-4	Sequence 4, Appl
33	906.4	11.2	4883	3	US-08-475-975-4	Sequence 4, Appl
34	906.4	11.2	4883	3	US-09-084-889-4	Sequence 4, Appl
35	906.4	11.2	4949	3	US-09-138-024-22	Sequence 22, Appl
36	906.4	11.2	5399	1	US-08-064-121-1	Sequence 1, Appl
37	906.4	11.2	5399	1	US-08-478-015-1	Sequence 1, Appl
38	906.4	11.2	5399	3	US-08-475-975-1	Sequence 1, Appl
39	906.4	11.2	5399	3	US-09-084-889-1	Sequence 1, Appl
40	906.4	11.2	5618	3	US-08-799-569-1	Sequence 9, Appl
41	906.4	11.2	5620	1	US-08-104-072B-9	Sequence 9, Appl
42	906.4	11.2	5620	1	US-08-351-413-3	Sequence 3, Appl
43	906.4	11.2	5620	2	US-09-025-583-3	Sequence 3, Appl
44	906.4	11.2	5642	1	US-08-318-772A-2	Sequence 2, Appl
45	906.4	11.2	5653	1	US-08-073-836-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-801-092-5
; Sequence 5, Application US/08801092
; Patent No. 6074850
GENERAL INFORMATION:
APPLICANT: Antelman, Douglas
APPLICANT: Gregory, Richard J.
TITLE OF INVENTION: Tissue Specific Expression of
TITLE OF INVENTION: Retinoblastoma Protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,092
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,517
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
AUTHOR/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 016930-001020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3853 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 209..250
FEATURE:
NAME/KEY: CDS

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LOCATION: 254..289
FEATURE:
NAME/KEY: CDS
LOCATION: 293..505
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NAME/KEY: CDS
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LOCATION: 518..520
FEATURE:
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LOCATION: 524..658
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NAME/KEY: CDS
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LOCATION: 695..748
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LOCATION: 752..781
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NAME/KEY: CDS
LOCATION: 785..829
FEATURE:
NAME/KEY: CDS
LOCATION: 1132..1134
FEATURE:
NAME/KEY: CDS
LOCATION: 1138..1149
FEATURE:
NAME/KEY: CDS
LOCATION: 833..862

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Query Match	15.3%;	Score 1240.4;	DB 3;	Length 3853;
Best Local Similarity	-74.1%;	Pred. No. 1.2e-267;		
Matches 191;	Conservative	0;	Mismatches 96;	Indels 573; Gaps 4;

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Oy	61	attacggygcattagtcatcagccacataatggagltcgcgltacataactc	120
Db	270	attacggggctattagttgattacatagcccatattatgtagtccgcttaca	325
Oy	121	aatggccgccttgctgacgccccaaagccccgcacattgagctcaataat	180
Db	330	aatggccgccttgctgacgccccaaagccccgcacattgagctcaataat	385
Oy	181	gtcccaatagtaaacgccacataggagcttccattgacgtcaatggtgga	240
Db	390	gttcccatagtaaacgccacataggagcttccattgacgtcaatggtgga	445
Oy	241	taaatctcccaacttggcagatcatcaagtgtatcatatatgcgaagta	300
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Oy	301	gtcaatgacgttaaatgccccgcctgctgacattatgccagtaacatga	360
Db	510	gtcaatgacgttaaatgccccgcctgctgacattatgccagtaacatga	565
Oy	361	cttacttggcagtaacatctacgtattagtaacgtcatatcaacatggt	420
Db	570	cttacttggcagtaacatctacgtattagtaacgtcatatcaacatggt	625
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Oy 1108 gagaagcggttctgcttggcgctcttcgccttcgcctcactgactgctgcgc 1167
Db 1890 GGAAGAGCGGTTTGCTATTGGCGCTTTCCTCCCTTCCTCGCTCACTGACTGCTCGCT 1949
Oy 1168 cgttctgcctgcctgcgcgcgcgtatcagctcaactcaaaagcggtatcaag 1227
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Oy 1228 cagaatcagggataacgacgaagaacatgtgacaaagccagccaaagccagga 1287
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Oy 1288 accgtaaaagccgcgtctgcgtcttctccatagctcgcgcgcgcgcgcgcgcgc 1347
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Oy 1348 acaaaaatcgaagctcaagtcgaagtggaacccgaacagactataagaatacagg 1407
Db 2130 ACAAAATCGACGCTCAAGTCAAGAGTGGCGAAACCCGACAGCATATAAATACAGG 2189
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Oy 1468 acctgcgcgccttctccctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1527
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Oy 1528 atctcagtcggttgtagtgcctcgcctcaagcgtggtcgtgcgcgcgcgcgcgc 1587
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Oy 1588 agcccgacgc 1647
Db 2370 AGCCCGACCGCTGCGCTTATCCGTAATCTGATGTCCTTGAATCAACCCGTAAGACAG 2429
Oy 1648 acttatcgccactgagcagcagccagtcgaacagagtagcagagcagagtagagcg 1707
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Oy 1708 gtgctacagagtccttgaagtggtgagcctaactacgcgtactagaagacagta 1767
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Oy 1768 gtatctgcgctctgctgaagcagcttaacttcggaaaagagtgtagctctgac 1827
Db 2550 GATATCGCCCTGTGCTGAAGCAGATACCTTCGAAAAAGAGTGTGATCTTGTATCCG 2609
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Oy 1888 gaaaaaagagatcacaagaatccttgcattcttctacggtgtcgcgcgcgcgcgcgc 1947
Db 2670 GAAAAAAGATCTCAAGAAATCTTTGATCTTTCTACGGGGCTGACGCTCACTGGA 2729
Oy 1948 acgaaaacacacagtgtagatcttgcctacagcagatacatattgaatgattaga 2007
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RESULT 2

US-08-801-092-19
Sequence 19, Application US/08801092

Patent No. 6074850
GENERAL INFORMATION:

APPLICANT: Antelman, Douglas
APPLICANT: Gregory, Richard J.
TITLE OF INVENTION: Tissue Specific Expression of
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,092
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,517
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 016930-001020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
INFORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 4026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 209..250
FEATURE:
NAME/KEY: CDS
LOCATION: 254..289
FEATURE:
NAME/KEY: CDS
LOCATION: 293..505
FEATURE:
NAME/KEY: CDS
LOCATION: 509..514
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NAME/KEY: CDS
LOCATION: 518..520
FEATURE:
NAME/KEY: CDS
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NAME/KEY: CDS
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LOCATION: 695..748
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NAME/KEY: CDS
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NAME/KEY: CDS
LOCATION: 833..862

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US-08-801-092-19

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Query Match	13.28;	Score 1068.6;	DB 3;	Length 4026;
Best Local Similarity	69.78;	Pred. No. 2.7e-229;		
Matches 1918; Conservative	0;	Mismatches 89;	Indels 746;	Gaps 5

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QY	61	atacggggtcatagttcatalagccatatatgagttlccggttacaaactagyla	120
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RESULT 3
US-08-760-615-7

Sequence 7, Application US/08760615
Patent No. 6200959
GENERAL INFORMATION:
APPLICANT: Haynes, Joel R
APPLICANT: Schmaljohn, Connie S
APPLICANT: Fuller, Deborah L
APPLICANT: Schmaljohn, Alan
TITLE OF INVENTION: GENETIC INDUCTION OF ANTI-VIRAL IMMUNE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:

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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/760,615
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Berson, Bennett J
? REGISTRATION NUMBER: 37094
? REFERENCE/DOCKET NUMBER: 110229, 91241
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 608-251-5000
? TELEFAX: 608-251-9166
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4326 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: circular
? MOLECULE TYPE: other nucleic acid
? DESCRIPTION: /desc = "Expression vector"
? IMMEDIATE SOURCE:
? CLONE: pMRG7077
? FEATURE:
? NAME/KEY: promoter
? LOCATION: 1250..2062
? FEATURE:
? NAME/KEY: Intron
? LOCATION: 2063..2887
? OTHER INFORMATION: /function= "Human Cytomegalovirus"
? OTHER INFORMATION: Intron A"
? FEATURE:
? NAME/KEY: polyA_site
? LOCATION: 2912..3314
? FEATURE:
? NAME/KEY: CDS
? LOCATION: complement (299..1114)
? US-08-760-615-7

Query Match 13.0%; Score 1053.6; DB 4; Length 4326;
Best Local Similarity 94.1%; Pred. No. 6.3e-226;
Matches 1118; Conservative 0; Mismatches 39; Indels 31; Gaps 1;

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Oy 1480 ttctccctcgggaagcgttgagcgtttcctcaatgctcaagcgtgtagtattcagtcgg 1539
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Db 4139 GTTAAAGGATTTGTGTCATGAGATTATCAAAAAGATCTTCAACCTAGA 4186

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RESULT 4
US-08-893-327-15
; Sequence 15, Application US/08893327
; Patent No. 6020192
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GENERAL INFORMATION:
; APPLICANT: Zolotukhin, Sergei
; APPLICANT: Hauswirth, William W.
; APPLICANT: Muzyczka, Nicholas
; TITLE OF INVENTION: Humanized Green Fluorescent Protein
; TITLE OF INVENTION: Genes and Methods
; NUMBER OF SEQUENCES: 20
;
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433

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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,201
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UFLA:062\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
;
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6253 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 988..1701
;
; US-08-893-327-15

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Query Match 12.1%; Score 981.8; DB 3; Length 6253;
Best Local Similarity 86.9%; Pred. No. 7.6e-210;
Matches 1162; Conservative 0; Mismatches 37; Indels 138; Gaps 2;

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Db 3077 COTCCCGGTGCTCTTGTGACCCCTGGAAGGTGCACATCCACATGCTCTTCTCTAATAA 3136
Oy 929 atgaagaaatgcatcgtcgtatgctgagtaagtgatcattcattccttcttgggggtg 988
Db 3137 ATGAGGAATTCATCGCATTTCTGAGTAGTGTGATCTTAATTTCTGGGGGTGGGTCG 3196
Oy 989 ggcagagacagaaagggggaagattggaagaacaatagcagcagcatgtctggga----- 1040
Db 3197 GGCAGGACAGCAAGGGGGAAGATTGGAGAACATAGCAGGCATGCTGGGAGAGATCTA 3256
Oy 1041 ----- 1040
Db 3257 GGAACCCCTAGATGATGATGGCCACCTCCCTGTGGCGGTGCTCGCTCATGAGGC 3316
Oy 1041 -----tgcggtggtctatagcttctgagcggaagaacag-- 1079
Db 3317 CGCCCGGCAAGCCCGGCGGTGCGGCGACCTTTGTGTCGCCGCTCAGTGAAGAGCG 3376
Oy 1080 -----ctgcattatg 1090
Db 3377 AGCGGCAAGAGAGGAGTGGCCACCCCGCCCCCGCCCCCTGACGCTGACATTAATG 3436
Oy 1091 aatcgccaacgcgcggggaagagcggttgcgtatgtggcgctcttcgctcctgcgt 1150
Db 3437 AATCGGCCAACCGCGGGGAGAGGGGCTTGTGATTTGGGCGCTTCTCCGCTTCTCCGCT 3496
Oy 1151 cactgactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1210
Db 3497 CACTGACTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3556
Oy 1211 ggtatacgtgtataccacaagaatcaggagataacgcaggaagaacaatgtagcaaaagg 1270

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Db 3584 GGTAAATCGGTTATCCACAGATATACGGGATTAACCGAGAAAGACATGTATGACAAAAAGG 3643
QY 1271 ccagcaaaagccaggaacgltaaaagccgctgtgctggcgtlttccaaaggtccg 1330
Db 3644 CCACGAAAGGCCAGGAACCGTAAAGAGGCCGCTGTGGCGTTTCCATAGGCTCCG 3703
QY 1331 cccccctgaagagcatcaaaaaatcgacgtcgaagtgcgaagtggcgaaacccgcaagg 1390
Db 3704 CCCCCCTGACGAGCATACAAAAATTCAGCTCAAGTCAGAGTGCGGAAACCCGACAGG 3763
QY 1391 actataagataccaggcgtttcccttgaaagcttccctgtgagccttccctgttccgac 1450
Db 3764 ACTATAAGATACCAAGCGGTTTCCCTCGAAGCTCCCTCGGCTCTCTGTTCCGAC 3823
QY 1451 cctgacgtaccaggaactgtccgccttccctccttggaagcgttgagccttccca 1510
Db 3824 CCTGCGCTTACCGGATACGTCGCGCTTCTCCCTTCGGAGAGCGTGGCGCTTTCGA 3883
QY 1511 atgtcaagctgtatgtatctcaagttcgggtgaagtgctgctcccaagctggcgtgt 1570
Db 3884 ATGCTCACGCTGTAGTATCTCACTGTGCTAGTGTGCTGCTCCAAAGCTGGGCTGTGT 3943
QY 1571 gcaagaaacccccgttgaagccccgcgctgagccttaccgtaactatgcttcttgaagc 1630
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QY 1631 caaccgcgtlaagacagactatcgcacactgagcagcagcactglaacagattagcag 1690
Db 4004 CAACCCGCTAAGACACAGACTTATGCGCACTGGCAGACGCCACTGTTAACAGATTAGCAG 4063
QY 1691 agcgaagtagtgagggcggtgtctacaagttccttgaagtgtgtgacctactacgtctaac 1750
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Db 4124 TAGAAGACAGATATTGTGATCTGCGCTGTCTGTAACCGCACTTCTTGGAAAAAGAGT 4183
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Db 4184 TGGAGCTCTTGTATCCCGCAAAACAAACACCGCTGTAGCGGCTGTTTGTGTTGCA 4243
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Db 4244 GCGACAAATTAAGCGCGCAAAAAAAGATCTCAAGAAATCTTGTGATCTTGTACGGG 4303
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Db 4304 GTCGAGCGTCAGTGGAAACGAACCTCAGCTTAAGGATTTTGGTCATGAGATTATCAAA 4363
QY 1991 attgaatgtattaga 2007
Db 4364 AAGGATCTTCACCTAGA 4380

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RESULT 6
US-08-893-327-19
; Sequence 19, Application US/08893327
; Patent No. 6020192
; GENERAL INFORMATION:
; APPLICANT: Zoelutukhin, Sergei
; APPLICANT: Hauswirth, William W.
; APPLICANT: Muzyczka, Nicholas
; TITLE OF INVENTION: Humanized Green Fluorescent Protein
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/588,201
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UFLA:062\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEO ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 988..1728
; US-08-893-327-19

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Query Match 12.1%; Score 981.8; DB 3; Length 6280;
Best Local Similarity 86.9%; Pred. No. 7.6e-210;
Matches 1162; Conservative 0; Mismatches 37; Indels 138; Gaps 2;

QY 809 ctaagcctcgatgtagcctcagctgctgctttagtgcgaacatctgtttggc 868
Db 3044 CTAGAGCTCGCTGATACGACCTGACGTGCTTATGTCACCACTCTGTGTTGCC 3103
QY 869 cctcccccgtccttcccttgaacctggaagtgccaactcccaactccttccataaa 928
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QY 1041 -----tgcgltggtctataggtcttctgaagcgggaagaaacag-- 1079
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Db 3404 AGCCGCGCAGAGGAGTGGCCAAACCCCGCCCGCCCGCCCTGACGCTGATTAATG 3463
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Db 3524 CACTGACTCGCTGCGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3583
QY 1211 gtaatacgtgtatccagatacaggaaggaataagcaggaagaaacatgtgaagaaag 1270

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Db 3584 GGTAATACGTTATCCACAGATCAGGGGATACGAGAAAGAACATGTGACCAAAAGG 3643
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Qy 1691 agcgaagatagtagcagtgctgacagagcttctgaagtggtgagcctaactacggtctaac 1750
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Db 4244 GCACAGATTAACGGCGCAAAAAAAGATCTCAAGAAAGATCTTGAATCTTTCACGGG 4303
Qy 1931 gtcgaagcctcagtggaagcaaaactcaagcttaagggatttgtagtagcgagatacat 1990
Db 4304 GTCTGAGGCTCAGTGAAGCAAAACTACGTTAAGGGATTTGGTATGAGATTAATCAAA 4363
Qy 1991 attgaatgtaattaga 2007
Db 4364 AAGGATCTTCACCTAGA 4380

RESULT 7

US-08-343-401A-3
Sequence 3, Application US/08343401A
Patent No. 5661132

GENERAL INFORMATION:

APPLICANT: Swain, William F
APPLICANT: Macklin, Michael D
APPLICANT: Eriksson, Elov
APPLICANT: Andree, Christophe
TITLE OF INVENTION: Improved Wound Healing
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady
STREET: PO Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,401A
FILING DATE: 22-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9103-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4283 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: pMRG1630
FEATURE:
NAME/KEY: exon
LOCATION: 713..721
FEATURE:
NAME/KEY: exon
LOCATION: 981..1253
FEATURE:
NAME/KEY: CDS
LOCATION: join(713..721, 981..1253)
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 713..1049
US-08-343-401A-3
Query Match 12.08; Score 973; DB 1; Length 4283;
Best Local Similarity 83.28; Pred. No. 6.1e-208;
Matches 1216; Conservative 0; Mismatches 30; Indels 215; Gaps 1;
Qy 762 ctgagacatgcatcgaagggccctatctatagtgtaacctaaatgtagagctgcgtg 821
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Qy 1075 ----- 1074
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Qy 1075 ----- 1074

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Db 2057 TCCGCCCCCTGACGAGCATCAAAAAATCGAGCTCAAGTCAAGAGTGGCGAAACCCGA 2116
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Qy 1927 cggggtctgagcgtcagtgagaaacgaacatcagtaaggaatttgatcagtcagat 1986
Db 2657 CGGGGTCTGAGCGCTCAGTGAAGAAACTCAGTTAAGGATTTTGGTCATGAGATTA 2716
Qy 1987 acatattgaaatgatttga 2007
Db 2717 CAAAAGGATCTTCACTAGA 2737

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US-08-445-265A-1
; Sequence 1, Application US/08445265A
; Patent No. 5697901
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Eiof
; TITLE OF INVENTION: GENE DELIVERY BY MICRONEEDLE INJECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,265A
; FILING DATE:
; CLASSIFICATION: 604
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 110229, 91080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Plasmid DNA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(713..721, 981..1250)
; US-08-445-265A-1

Query Match 12.0%; Score 973; DB 1; Length 4283;
Best Local Similarity 83.2%; Pred. No. 6,1e-208;
Matches 1216; Conservative 0; Mismatches 30; Indels 215; Gaps 1;

Qy 762 ctcgagcatgcatctagaagggccctatctatagtgtaaccctaaatgctagagctgctg 821
Db 1277 CTCGACATGCATCTTAGAGGGCCCTATTCTATAGTGTCACTAAATGCTAGAGCTCGCTG 1336
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Qy 1075 ----- 1074

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Db	1637	AAATCATGGTAAATACAGCTTTTCCTGCTGTGAATTTGTTATTCGGCTCAACAATTCACACACA	1636
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Db	1997	AAGCGCAGCAAAAGCCAGGAACCGTAAAAAGGCCCGTCTGGCGTTTTTCATATAGC	2056
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Qy	1507	ctcaagtctcaagctgtatgtagtattcctaagttcggtgttagtgcgttcgctccaagctggct	1566
Db	2237	CTCATACCTTACACGCTGTAGGTATCTCATGTTCCGTTAGTTCCTTCGCTCCAAAGCTGGCT	2296
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Qy	1627	agltccaaccccggttaagacacagacttatcgccacttgcagtcagcaaccaactgtttaaagatt	1686
Db	2357	AGTCCAAACCCGGTAAAGACAGACTTATTCGCCCACTGGCAGACACCACTGGTAAACAGATT	2416
Qy	1687	gcagagcagaggtatgttagcggtgtcctacagagttccttgaagtgtgtgccttaactaagct	1746
Db	2417	GCAAGCGAGAGTATGTAGGGGGGTCTACAGAGTTCCTTGAAAGTGGGGCTTAACTAACGCT	2476
Qy	1747	acaatagaagaagaatatttggatcttgatctgscctctctgaagccaatlaactcttgaaaaa	1806
Db	2477	ACACTAACAGACAGATTTTGGTATCTGGCGCTCTGTGAAGCAACTTACCTTCGGAAAA	2536
Qy	1807	gaattgttagctcttgatcccggaacaaaccaacgcctgtgtatgtagcggttggtttttggtt	1866
Db	2537	GAGTGTGTACTCTTATATCCGGCAACCAACCAACGCGCTGTATGGCGTGTGTTTTTGT	2596
Qy	1867	gcaagcagcagatlaecgcgcagaaaaaaagatctcaagaagatccctttagtctttctta	1926
Db	2597	GCAAGCAGCAGATATACCGCGAGAAAAAAGATATCTCAGAAAMANTCTTTGATCTTTTCT	2656
Qy	1927	cgaggctctgcgcctcagttgtaacgaacaaactcagtttaagggatttggttcatgtagcgat	1986
Db	2657	CGGGGCTTGACCTCACTGGAACGAAACTCACGTTAAGGATTTTGGTCACTGAGATTAT	2716
Qy	1987	acacattgaatglatlatta 2007	

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Db      2717  CAAAAGAGCATCTTCACCTAGA 2737

RESULT          9
US-08-990-442-1
: Sequence 1, Application US/08990442
: Patent No. 6090790
:
: GENERAL INFORMATION:
: APPLICANT: Eriksson, Elof
: TITLE OF INVENTION: GENE DELIVERY BY MICRONEDDLE INJECTION
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Charles & Brady
: STREET: 1 South Pinckney Street
: CITY: Madison
: STATE: WI
: COUNTRY: US
: ZIP: 53703
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/990,442
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Beison, Bennett J
: REGISTRATION NUMBER: 37094
: REFERENCE/DOCKET NUMBER: 310558.90028
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 608-251-9166
: TELEFAX: 608-251-9166
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4283 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: circular
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "plasmid DNA"
:
: FEATURE:
: NAME/KEY: CDS
: LOCATION: join(713..721, 981..1250)
:
US-08-990-442-1

Query Match          12.0%; Score 973; DB 3; Length 4283;
Best Local Similarity 83.2%; Pred. No. 6,1e-208;
Matches 1216; Conservative 0; Mismatches 30; Indels 215; Gaps 1;

OY      762  ctcaagcatgatcatcagaagggcccatctatctatagtgtaaccctaataatgtagagctcgctg 821
        |||||
Db      1277  CTCGAGCATGCAATCTAGAGGGCCCTATTCTATGATGTCACCTAAATGCTAGAGCTCGCTG 1336

OY      822  atcagccctcgaactggtccctctagtgtgcagaaccatctgttlttgccctcccccgtgac 881
        |||||
Db      1337  ATCAGCCCTCGAATGTGCGCTTCTAGTGTGCAAGCAACATCTGTTGTTGCCCTCCCGGTGCC 1396

OY      882  ttccctgaacctggaaggtgcacatcccaactgcctcttcctctaataatgagaaattgc 941
        |||||
Db      1397  TTCCTTGACCCCTCGAAGGTCGCACATCCCACTGCTCTTCTTAATATAATGAGGAATATGC 1456

OY      942  atcgcatgtctgtagttagtgcatactatctcgtgggggtgggtggggcaggaagcaaa 1001
        |||||
Db      1457  ATTCGATTTGCTGATGATGATGTCATTCATTCGTGGGGGGTGGGGGGGAGCAAGCA 1516

OY      1002  gggggagagatgaggaagcaaatagcaagcagctggtggatgcggtgggctctatgcttc 1061
        |||||
Db      1517  GGGGGAGGATTTGGGAAGCAATAGCAGGCATGCTGGGATGCGGTGGGCTCATGTGAAC 1576

OY      1062  tgaagcggaagaa----- 1074

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Db 1577 AGCTGGGGCTCGAGCATGCAAGCTTGAGTATTCTATAGTGTCACTAAATAGCTTGGCGT 1636
Qy 1075 ----- 1074
Db 1637 AATCATGTGTCATAGCTGTTCTGTGTGAATTTGTTATCCGTCAATTCACACANCA 1696
Qy 1075 ----- 1074
Db 1697 TACGAGCCGGAAGCATTAAGTTAAAGCTGGGGTGCCTAATGACTGACTAATCACTACAT 1756
Qy 1075 ----- accagctgcat 1086
Db 1757 TAATTGGGTGCGCTCACTGCGCGCTTTCACACTCGGGAACCTGTGCGCCAGCTGCATTT 1816
Qy 1087 aatgaatcgcaacgcgcggggaaggcggttgctgattggcgctcttcctccgtctc 1146
Db 1817 AATGAATCGCCAAAGCGCGGGGAGAGCGGTTTGCCTATTGGGGCGCTTCCGCTTCC 1876
Qy 1147 cgcctcactgactcgctgcgcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttc 1206
Db 1877 CGCTCAGTCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1936
Qy 1207 aggcgtaatacggltatccacagaatcaggaggtataacgcaggaagacaatgtgacaa 1266
Db 1937 AGCGGGTATACGGTTATCCACAGATCAGGGGATACGCAAGGAAGAACATGTAGCAA 1996
Qy 1267 aagcccgcaaaaaggccaggaacgcgttaaaaagccgcgttcgttcgttcgttcgttcgttc 1326
Db 1997 AAGGCCACCAAAAGGCCAGGAACCGTAAAGGCCGCTTCTGCTGCTTCTTTCGATAGGC 2056
Qy 1327 tccgcccccccgagcagatcacacaaaatcgacgctcaagtcagaggggggcaaacccga 1386
Db 2057 TCCGCCCCCTCGAGAGAGATCACAAAATCCAGCGCTCAAGTCAGAGGTCGGAACCCGA 2116
Qy 1387 caggactataaagataccagagcglttcccccgtgaagctccctcgctgcctcctgttc 1446
Db 2117 CAGACATATAAGATACAGAGCGTTTCCCTCGAGAGCTCCCTGCTGCTGCTGCTGCTGCTG 2176
Qy 1447 cgaccctgcgcgttacccgatacgtgttcgcgtcttctcccttcgttggaagcgttgagcttc 1506
Db 2177 CGACCTGCGCGCTTACCGGAATCCTGTGCGCTTCTTCTTCCGGAAGCGTGGCGCTT 2236
Qy 1507 ctcaatgcctcagcgttgatgatcctcagctgcgttgatgctgcgttcagcctcagcctgcgt 1566
Db 2237 CTCATAGCTCAGCGTGAATGATCATCATGTTGGGTAGTGTGCTTCGCTCAAGCTGGGCT 2296
Qy 1567 gtgtgacagaaaccccccggttccagccgcgcgcgttcgcttaccgtaatacgtcttg 1626
Db 2297 GTGTGACAGAAACCCCGTTACGCCCGCTGCGCTTATCCGTTAACTATCGCTT 2356
Qy 1627 agtccaaacccggaagaacagactatcgcaactgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1686
Db 2357 AGTCCAAACCCGTTAAGACACACTTATCGCACTGCGAGCAGCCACTGTGTAACAGGATTA 2416
Qy 1687 gcagaagcaggtatgtgagcggttcacagagttcttgaatgggtgagcctaactagcgt 1746
Db 2417 GCAAGAGGAGTATGTAGCGCGCTCTACAGAGTCTTGAATGGTGGCCTAATCACTAGGCT 2476
Qy 1747 acactaagaagacagatltgtgatactgcgcgttcgttcgaagccagltacacttcggaana 1806
Db 2477 ACACTAAGAAGACAGTATTTTGGTATCTGCGCTCTGCTGAACCCAGTTACCTTCGGAANA 2536
Qy 1807 gaagtgtgtagctcttctgttcgggaacaacacacgcgcgttggtgaagcgttggttttttt 1866
Db 2537 GAGTTGTTACTCTTTGATCCGGCAAAACACACCGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 2596
Qy 1867 gcaagcgcagattacgcgcgaanaaaagatctcaagaagatcccttgaatcttcttcttctt 1926
Db 2597 GCAAGCAGCAGATTAACCGCAGAAAGAAAGATCTCAAGAAAGATCTTGTATCTTTTCTA 2656
Qy 1927 cggggttcgacgctcagtggaacgaanaactcaglttaaggagatltgtgatacgaagcgt 1986
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Db 2657 CGGGGTCTGAGCCCTCAGTGGGAACGAAGAACTCAGTTAAGGATTTTGTGTCATGATTAAT 2716
Qy 1987 acatatgtgaatgtattaga 2007
Db 2717 CAAAAGGATCTTACACTAGA 2737

RESULT 10
US-09-082-649B-83
; Sequence 83, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 3987
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid pUK21-72
US-09-082-649B-83

Query Match 11.9%; Score 968.2; DB 4; Length 3987;
Best Local Similarity 85.9%; Pred. No. 7e-207;
Matches 1154; Conservative 0; Mismatches 33; Indels 156; Gaps 1;

Qy 796 tgtcaactaaatgtcagacgtcgtcgtatcagcctcgtacgtgtccttctagtgtccagcca 855
Db 40 tctcagactagacatgacgtcgtcgtatcagcctcgtacgtgtccttctagtgtccagcca 99
Qy 856 tctgtgtgttccctcccccgtgcttcttcccttgaacccgggaagtgccactccactgtc 915
Db 100 tctgtgtgttccctcccccgtgcttcttcccttgaacccgggaagtgccactccactgtc 159
Qy 916 ctctcctaataaataatgaagaatcgcgcgtatgtctgtgaatgagtgatcattctatctg 975
Db 160 ctctcctaataaataatgaagaatcgcgcgtatgtctgtgaatgagtgatcattctatctg 219
Qy 976 ggggggtggtgtgaggcagacagcagggggaagatgtggaagacaatagcagcgtct 1035
Db 220 ggggggtggtgtgaggcagacagcagggggaagatgtggaagacaatagcagcgtct 279
Qy 1036 gggggtggtgtgaggcgtcattggtc----- 1058
Db 280 ggggaagccttcgactagtggtcgtlaatcattgcatagctgttccgtgtgaatgtc 339
Qy 1059 ----- 1058
Db 340 tatccgtccaaattccacacaaatacagcgcgcggaagacataaagtgtaaagcgtgg 399
Qy 1059 -----t 1059
Db 400 gtgcctaattgtgagcctaactacatattgtgtgtgcgtcactgcgcgttccagct 459
Qy 1060 tctgaagcggaaagaacacgtcgtcattaaatgaatcgcgcgaacgcgcggggaagcgtgt 1119
Db 460 cgggaacactgtcgtccagcgtgcatatgaatcgcgcgaacgcgcggggaagcgtgt 519
Qy 1120 tgcgtattggcgctcttcgcctccgcgtcactgactgcgtgcgtcgtgtcgttcgtgcgc 1179
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[illegible]

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: CURRENT FILING DATE: 1998-05-20
: PRIOR APPLICATION NUMBER: US 60/047,233
: PRIOR FILING DATE: 1997-05-20
: PRIOR APPLICATION NUMBER: US 60/047,209
: PRIOR FILING DATE: 1997-05-20
: NUMBER OF SEQ ID NOS: 85
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 84
: LENGTH: 3987
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: plasmid pGT
: US-09-082-649B-84

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Query Match	11.98;	Score 961.8;	DB 4;	Length 3987;
Best Local Similarity	85.68;	Pred. No. 1.9e-205;		
Matches 1150; Conservative	0;	Mismatches 37;	Indels 156;	Gaps 1

[illegible]

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Db 820 gaagctccctcgtgctctcctcgtctccgaaccgcgcgttaaccggtatctcgtcc 879
QY 1480 ttcccccctcggaagcgttgcgtcttctcgaatgcctcaacgcttaagatctcgttcg 1539
Db 880 ttcccccctcggaagcgttgcgtcttctcgaatgcctcaacgcttaagatctcgttcg 939
QY 1540 ttagtgcgttcgtctcgaagcgttgcgtcttgcgaagcgttgcgttcgaacgcgt 1599
Db 940 ttagtgcgttcgtctcgaagcgttgcgtcttgcgaagcgttgcgttcgaacgcgt 999
QY 1600 gcgcctatccgcgttaacatctgcttgaagcgttgcgaagcgttgcgaagcgttgcga 1659
Db 1000 gcgcctatccgcgttaacatctgcttgaagcgttgcgaagcgttgcgaagcgttgcga 1059
QY 1660 tggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1719
Db 1060 tggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1119
QY 1720 tcttgaagctggtgcttaactaactaactaactaactaactaactaactaactaacta 1779
Db 1120 tcttgaagctggtgcttaactaactaactaactaactaactaactaactaactaacta 1179
QY 1780 tgcgtgaagcagcttaactcctcggaagagcttgcgtcttgcgtcgcgcgcgcgcgcgc 1839
Db 1180 tgcgtgaagcagcttaactcctcggaagagcttgcgtcttgcgtcgcgcgcgcgcgcgc 1239
QY 1840 ccgcctgtagcgttgcgttcttgcgtcagcagcagcagcagcagcagcagcagcagcag 1899
Db 1240 ccgcctgtagcgttgcgttcttgcgtcagcagcagcagcagcagcagcagcagcagcag 1299
QY 1900 ctcaagaagatccttgcgttcttgcgtcagcagcagcagcagcagcagcagcagcagc 1959
Db 1300 ctcaagaagatccttgcgttcttgcgtcagcagcagcagcagcagcagcagcagcagc 1359
QY 1960 gtiaggagatttgcgtcagc 1982
Db 1360 gtiaggagatttgcgtcagc 1382

```

RESULT 12

US-08-467-420A-49
Sequence 49, Application US/08467420A
Patent No. 5683892

GENERAL INFORMATION:

APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITL OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,420A
FILING DATE:
CLASSIFICATION: 536

```

PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/363131
: FILING DATE: 23-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Sutfon, Jeffrey A.
: REGISTRATION NUMBER: 34,028
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610 270-5024
: TELEFAX: 610 270-5090
: INFORMATION FOR SEQ ID NO: 49:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6285 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
US-08-467-420A-49

Query Match 11.4%; Score 921.8; DB 1; Length 6285;
Best Local Similarity 82.9%; Pred. No. 1.9e-196;
Matches 1160; Conservative 0; Mismatches 27; Indels 212; Gaps 1;

QY 821 gatagcctgcagctgctccttctagtgccagcagcagcagcagcagcagcagcagcagc 880
Db 3829 GATCAGCCCTGACACTGCTCTTCTAGTTGCGCAGCCATCTGTTGGCCCTCCCTCCCTGC 3888
QY 881 ctctcctgacctggaagcgtccactccactgctcctcctcctcctcctcctcctcctcctc 940
Db 3889 CTTCCTTGACCTTGGAAGGTGCCACTCCACTGCTCTTCTTCTATTAATGAGGAATTG 3948
QY 941 catgcactgctcgtagtagtgctcctcctcctcctcctcctcctcctcctcctcctcctc 1000
Db 3949 CATGCATCTGCTGAGTAGTGATCTATTCTGCGGGGTGGGGGAGGAGCAGACAGCA 4008
QY 1001 agggggagagatggaagacaatagcagcagcagcagcagcagcagcagcagcagcagc 1060
Db 4009 AGGGGAGAGATTGGGAGACAAATAGCAGGATGCTGGGGATGGGTGCTTATGGAAC 4068
QY 1061 ctgagcgcggaaga----- 1074
Db 4069 CAGCTGGGGCTCATTCAGTGTATGACTGGCGCCGATCCCGTGCAGACTTGGCTAA 4128
QY 1075 ----- 1074
Db 4129 TCATGTATAGCTGTTCTCTGTGTAATTTATCCGCTCAATTCACAAACATA 4188
QY 1075 ----- 1074
Db 4189 CGAGCCGGAAGCATMAAGTAAAGCCTGGGGTCCCTAATGAGTAGACTACACATTA 4248
QY 1075 ----- 1088
Db 4249 ATTGCTGTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1088
QY 1089 tgaatcgccaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1148
Db 4309 TGAATCGCCCAACGCGCGGGAGAGGCGGTTGGTATGGGCGCTTCCGCTCCCTCG 4368
QY 1149 ctcaactgactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1208
Db 4369 CTCACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4428
QY 1209 gcggttaacggtatccacagaatcaggggataacgcaggaagaacatgtagcaaaa 1268
Db 4429 GCGGTATACGTTATCCAGATCAGGGGATACAGGAAGAAGACATGTAGCAAAA 4488
QY 1269 ggcagcaaaaagcgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1328
Db 4489 GGCAGCAAAAAGCAGAGAACGTAATAAGCCGCTGCTGCGGTTTTCATAGGCTC 4548
QY 1329 cgcgccctcagcagcagcagcaaaaatcgaagctcaagtagcagagtgcgcaaacccgaca 1388

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|||||
Db 4549 CGCCCCCTGACGAGATCAAAAAATCGACGCTCAAGTCAAGAGTGGCCAAACCCACA 4608
Qy 1389 ggcataaagataccagcggttccccctggaaagctccctcgtcgtcctcgttcgcg 1448
Db 4609 GGAATATAAAGATACCAAGCGGTTTCCCGCTGGAAGCTCCCGTGGCGCTCTCGTTCGG 4668
Qy 1449 accctgcgtttaccgatacctcgttcctccttcccttccttccttccttccttccttc 1508
Db 4669 ACCCTGCCGCTTACCGGATACCTCTCCGCTTCTCCCTTCGGGAAACGGCGCTTCT 4728
Qy 1509 caatgcacacgctgtaagatctcagctcgttgaagtcgttcgttcctcctcctcctcgt 1568
Db 4729 CAATGCTACAGCTGTAGTATCTAGTTCGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 4788
Qy 1569 gtgcagacaccccgcttcagcccgacgctgcgcttacccttccttccttccttccttc 1628
Db 4789 GTGCACGACACCCCGCTTCAAGCCCGACCGCTGCGCTTATCCGGTACTATCTGCTGAG 4848
Qy 1629 tccaccccgtaagacacgactatgcacactgacacgacacgacacgacacgacacgac 1688
Db 4849 TCCACCCGGTAAAGACACGACTTATCGCACTGGACACGACGACGACGACGACGACGACG 4908
Qy 1689 agagcagatgtagagcggtgctacagagcttctgaagtcgttcgttccttccttccttc 1748
Db 4909 AGAGCGAGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGTGTAGTGTAGTGTAGTGTAG 4968
Qy 1749 actagaagacagatattgtatctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1808
Db 4969 ACTAGAAGACAGTATTTGTATCTGCGCTCTGCTGAAGCCAGTACTTTCGGAAGAAAGA 5028
Qy 1809 gtgtgagctcttgatccggaacacacacacacacacacacacacacacacacacacacac 1868
Db 5029 GTGTGAGCTCTTGATCCGCAACACACACACACACACACACACACACACACACACACACAC 5088
Qy 1869 aagcagacagatcagcgacagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 1928
Db 5089 AAGCAGCAGATTAAGCGCAGAAAAAAGATCTCAAGAGATCTTGTATCTTTCTTACG 5148
Qy 1929 ggtgtgagcctcagtgagacagaaactcagtgtaaggaatttggtcagagagagagac 1988
Db 5149 GGGTGTACGCTCAGTGAAGCAAACTCAAGTTAAGGATTTGTATGATGATGATTTATCA 5208
Qy 1989 atattgatactataga 2007
Db 5209 AAAAGATCTTCACTAGA 5227
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RESULT 13
US-08-470-110A-49
Sequence 49, Application US/08470110A
Patent No. 5693323

GENERAL INFORMATION:

APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TREATMENT OF ALLERGIC DISORDERS
NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSER: Intellectual Property
STREET: P. O. Box 1539-UM220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110A
FILING DATE:
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 6285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-470-110A-49
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Query Match 11.4%; Score 921.8; DB 1; Length 6285;
Best Local Similarity 82.9%; Pred. No. 1.9e-196;
Matches 1160; Conservative 0; Mismatches 27; Indels 212; Gaps 1;

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Qy 821 gataagcctgactgctgctcctcagtgacagcactgtgtgttgccctcccccgtgc 880
Db 3829 GATCAGCCTTGAGCTGCTTCTTGTAGTGCACGACATCTGTTGTTGCCCTCCCGTGC 3888
Qy 881 ctcccttgaccccggaagtgccacacacacacacacacacacacacacacacacacacac 940
Db 3889 CTTCCTTGACCTCGAAGGTCACCTCCACTGCTCTTCTTAATAAAGAGAAATG 3948
Qy 941 cctcagctgctcgtgagtgatcctcctcctcctcctcctcctcctcctcctcctcctc 1000
Db 3949 CATCGCATCTGATGAGTGTGATCTATCTCTGCGGCGGTGCGGCGGCGGCGGCGGCGG 4008
Qy 1001 aggggagagatggagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 1060
Db 4009 AGGGGAGAGATGGAGAAATGACAGCATGCTGGGAGTGGGAGTGGGAGTGGGAGTGG 4068
Qy 1061 ctgagcggaaga----- 1074
Db 4069 CAGCTGGGGCTGATGAGTGTGATGACTGGGCGCGCATCCGTCGAGACTTGGCGTAA 4128
Qy 1075 ----- 1074
Db 4129 TCATGTGATAGCTGTTTCTGTGTGAATTTATTCCTCCCTCAAAATCCACAAACATA 4188
Qy 1075 ----- 1074
Db 4189 CGAGCCGGAAGCATTAAGTAAAGCTGGGGTGTCTTAATGAGTGAAGTAACTCACTTA 4248
Qy 1075 ----- 1074
Db 4249 ATTGCGTGGCTGATCAGTCCCGCTTTCATCGGGAACCTGTGTCGACGCTGCAATTA 4308
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Db 5089 AAGCAGCAGATTAACGCCCAAAAAAAGGATCTCAAGAAATCTTGTATCTTTCTACG 5148
Qy 1929 gggctcagcgtcagtggaacgaactcaacgttgaaggtattgtgtcatgagcgatc 1988
Db 5149 GGGCTCAGCCTCAGTGGAAAGAAACTCAAGTTAAGGATTTTGTGTATGATTAATCA 5208
Qy 1989 atattgaatgattaga 2007
Db 5209 AAAAGATCTTCACCTAGA 5227

RESULT 14
US-08-667-769A-49
; Sequence 49, Application US/08667769A
; Patent No. 5783184

GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P.O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,769A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17082
FILING DATE: 22-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEO ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 6285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-667-769A-49
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Best Local Similarity 82.9%; Pred. No. 1.9e-196;
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OY 1989 atattgaaatgattaga 2007
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 01:01:13 ; Search time 5541.26 Seconds
(without alignments)
19765.864 Million cell updates/sec

Title: US-09-778-516A-1

Perfect score: 8115

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*
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4: em_estmu:*
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15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	719.2	8.9	724	AL645114	AL645114
5	708	8.7	800	AJ281449	AA3A-P45
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17	663.2	8.2	669	AL660789	AL660789

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23	652.2	8.0	657	9	AL641508	AL641508	
24	650.8	8.0	659	9	AL643220	AL643220	
25	649.8	8.0	680	9	AL646751	AL646751	
26	648	8.0	668	9	AL637190	AL637190	
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38	621.2	7.7	650	9	AL639359	AL639359	
39	615.2	7.6	718	12	AG010489	AG010489	
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42	608.8	7.5	632	9	AL638320	AL638320	
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44	606.8	7.5	687	9	AU001481	AU001481	
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ALIGNMENTS

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DEFINITION DKFZP434C172 3', mRNA sequence.
ACCESSION AL044364
VERSION AL044364.1 GI:5432586
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 954)
Ansoerge,W., Benes,V., Krieger,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Ansoerge, Benes, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Ansoerge W

MIIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No r1 sequence available.
This clone (DKFZP434C172) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubneweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
Location/Qualifiers
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DB 1038 TTTTGTGTTGTC-AGCAGACATTAACGCGC 1067
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LOCUS A0081124 Oncorhynchus mykiss Kidney infected by infectious
DEFINITION hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KG12,
mRNA sequence.
ACCESSION A0081124
VERSION A0081124.1 GI:6431472
KEYWORDS EST.
SOURCE rainbow trout.
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1089)
Kono,T., Sakai,M. and Lapetra,S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
JOURNAL Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1-nishi gakuenibadanai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES
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DEFINITION mRNA sequence.
ACCESSION AL645114
VERSION AL645114.1 GI:16797239
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodidae; Silurana.
REFERENCE 1 (bases 1 to 724)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001
Unpublished (2001)
JOURNAL Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE.ID: TNeu017b19.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
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/note="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; CDNA
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EcoRI-NotI cut cDNA was then ligated into PCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT      162 a      206 c      194 g      162 t
ORIGIN

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Query Match	8.9%	Score 719.2	DB 9	Length 724
Best Local Similarity	99.6%	Pred. No. 2.2e-168		
Matches 721; Conservative	0	Mismatches 3	Indels 0	Gaps 0

OY 1145 ctcgcctcaactgacgtcgtcgctcgagtcggtcgtcgatcgagcgatatacgaactcatc 120

Db 1 CTCGCTCAACTGACTCGCTCGGTCTGGTTCGGCTCGGCAGCAGCGATACACTCACATC 60

Qy 1205 aaagggcgtataacggtatccacagaaatcagggataacgcaggaaagaacatgtgagc 1264
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Db 61 AAAGGGCGTATACGGTTATCCACAGAAATCAGGGGAAACGCAAGGAAGACATGTGACC 120

Qy 1265 aaaagcgccagcaaaagccgaacctaataaagcgccgctttttccatag 1324
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 Db 121 AAAAGCCAGCAAAAGCCAGGACCGTAAAAAGCCCGCTTGCGTTTTCATAG 180

QY 1325 gctccgccccctgacgagcatcaacaaatcgaagtcagagtgcgcaaaccc 1384
|||||
Db 181 GCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGCTGGCAAAACC 240

QY 1385 gacgcgactataagatacaccagcgcttcccccgtgaagctccctcgtgacgtctctcgt 1444
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Db 241 GACGCGACTATAAGATACCAAGCGCTTTCCCCCTGGAGCTCCCTCGTGGCGCTCTCCTGT 300

QY	1445	tcgcgaacctgycgcttacgcgatacctgtccgccttctcccttcgggaagcgtgacgt	1500
Db	301	TCGCACCCCTGCCGCTTACCGGATACTGTCCGCCCTTTCCTTCGGGAAAGCGTGGCCGT	360

QY 1505 ttctcaatgctcagctgttagtattctcagttcggtagtgcgttcgccccaagctggg 156
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 TTCTCATAGCTCACCGGTGATGATTCTCAGTTTCGGTGTAGTGCTTCGCTCCAAAGCTGGG 420

QY 1565 ctgtgtgcacgaacccccgcgttcagcccgacgcgtgcgcctataccgtaactatcgtct 1624

QY 1625 tgagtcacaaccggtgaagacacgacttatacgcactctgcagcagccacttgttaacagat 1684
|||||
Db 481 TGAGTCCACACCGGTGAAGACACGACTTATCGCCACTGCAGCAGCCACTGGTAAACAGAT 540
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Oy 1685 tagcagagcaggtatgttaagcgtgctacagaagttcttgaagtgtgacctactacg 1744
|||||
Db 541 TAGCAGAGCGGATGTGTAGCGGCGGTGTACAGAGTCTTGTGAAGTGGTGGCGCTACTACGG 600
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QY 1745 ctacactagaagacagltattgttctcgcctctcgtgaagccagttaccttcgaaa 1804
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 DB 601 ctacactagaagacagltattgttctcgcctctcgtgaagccagttaccttcgaaa 660

[illegible]

QY 1865 ttgc 1868
1111

20 121 100 121

RESULT 5

Accession	Length	Type	Release Date
AF261443	800 bp	mRNA	Linear
LOCUS			EST 30-JUN-2000

DEFINITION	4A3A-4AD5-F Anopheles gambiae immune competent 4A3A Anopheles gambiae CDNA clone 4A3A-4AD5, mRNA sequence.
ACCESSION	AJ281449
VERSION	AJ281449.1
KEYWORDS	GI:6929329
SOURCE	EST.
ORGANISM	African malaria mosquito. Anopheles gambiae

REFERENCE

Danişoglu, Necatigözü, Hacıoğlu, Kayaalp, Öner, Özdemir, Şenel, Şengül, Şimşek, Tuncer, Yılmaz, Zengin, Zeynelabidin, Zorlu, and Zorlu. 2009. Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae 1 (bases 1 to 800) ; Anopheles.

TITLE	AUTHORS
Anopheles gambiae pilot gene discovery project: identification of	Donohue, S., Casasnovas, J., Vaurio, J., Conceicao, J., Soares, M.B., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansong, W., Soares, M.B. and Kafatos, F.C.

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE
20300950

COMMENT
Contact: dimopoulos g
Fotis C. Kafatos Laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.

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FEATURES
source
location/Qualifiers
1. .800
/organism="Anopheles gambiae"
/strain="AA r/r"

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/adb_xref="caxon:/165"
/clone="4A3A-P4D5"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/cell_line="immune competent 4A3A"

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/lab_host="E. coli DH10B" (pharmacia) with a modified
/notes="Vector: pT7T3D-Pac polylinker: Site 1: EcoRI Site 2: NotI; sequenced from
forward priming site which reads from the 3' end of the

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oligo-T primed cDNA according to: Bonaldi, Lennon & Soares (1986). Normalization and Subtraction: Two approaches to

BASE COUNT	203 a	206 c	198 g	193 t	Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN					

Query Match	8.7%	Score 708	DB 9	Length 800
Best Local Similarity	96.7%	Pred. No. 1.5e-165		

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QY 1320 cataggctcgcgccccctgacgagcatcacaaaaatcgacgctcaagtcagaggtggcga 1379

QY 1380 aaccgcagagactataagaataccagcgcttcccccgtgaagctccctggtgcctc 1439

QY 1440 cctgttccgacctgcccgttaccgataacctgcccgccttcccttcgggaagcgtg 1499

DB 192 CCGTCTCCGACCCCTGCCCCCTACCGGATACCTGTCGCCCTTTCCTCCCTTCGGGAGAGCG 231

QY 1500 GCGCTTCTCAATGCTCAAGCTGATGATCTCAATCTCGTGTGAGTCTGCTCGCTCCAA 1559

DB 252 GCGCTTCTCATAGCTCAAGCTGATGGATACATTCGGGCGTAGGTCGTTCCCTCCAG 311

QY 1560 ctggagctgtgtgacgaagcccccttcagcccgacccgtgcgccttaaccgtaacct 1619

Db 312 CTGGGGCTGTGTGACGAAACCCCCCGTTTCAGGCCGACGCTGCGCCTTATCCGGSTAACATAT 371

Qy 1620 cgtcttgagttccaaaccggttaagacaagcaacttcgtcccaactgtgcagcagcccaactgtgtac 1679

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Db 372 CGCTGAGTCCACCCGCGTAAGACACGACTTATCGCCACTG6GACAGCACCACCTGCTAAC 431
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Db 432 AGGATTAGCAGAGCAGAGGATATAGCGGCTGCTACAGAGTTCTTGAAGTGCGCTTAC 491
Qy 1740 tacggctacacagagagacagatttggtatctgcctgcctgtgaagccagttacttc 1799
Db 492 TACGGCTACACTAGAAAGAACAGTATTGGTATCTGCGCTGTGAGAGCCAGTTACCTTC 551
Qy 1800 ggaataaagagttgtagctcttgatccggcaacaacaacacccgctgtagcggtgtttt 1859
Db 552 GGAATAAAGAGTTGAGTCTTGATCCGCGAACAACAACCCGCTGTGAGCGGTGTTT 611
Qy 1860 ttgtgttcaagcagcagattacgcgcgaataaagagttccaagaagatccttgatc 1919
Db 612 TTTGTTTGCAGACACAGATTACGCGCAGAAAAAAGAGATCTCAAGAGATCTTTGATC 671
Qy 1920 ttctcaggggtctgacgctcagtggaacgaatacctcgttaagagatttgatcgt 1979
Db 672 TTTTTCAGCGGCTGTGACCTCAGTGGAACGAAACTCAGTTAAGGATTTTGGTCATG 731
Qy 1980 agcggatacatattgaatgattaga 2007
Db 732 AGATTATCAAAAAGATCTTCACCTAGA 759

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RESULT 6

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AL661706 715 bp mRNA linear EST 13-DEC-2001
LOCUS AL661706 XGC-neurula silurana tropicalis cDNA clone TNeu049m20 5',
DEFINITION mRNA sequence.
ACCESSION AL661706
VERSION AL661706.1 GI:17676434
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 715)
AUTHORS Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu049m20.sp6
Sequencing primer: Sp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
1..715
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu049m20"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

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FEATURES

source

BASE COUNT

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154 a 209 c 196 g 156 t

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ORIGIN

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Query Match 8.7%; Score 703.6; DB 9; Length 715;
Best Local Similarity 99.4%; Pred. No. 1.8e-164;
Matches 706; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 1076 ccaagctcatatgaatcggccaacgcyggggaagagcggttgcgtatgtggcgtc 1135
Db 6 CCAAGCTCATATGAAATGCGCCACGCCGGGAAGAGCGGTTTGCATTTGGCGCTC 65
Qy 1136 ttccgcttcctgcctcactgaactgcgtgcgtcgtcgttgcgtcgtgcgagcggtatc 1195
Db 66 TTCGCGTTCCTCGCTCAGTACTGCGTGGCGCTGGTTCGTTCCGCTCGGGGAGCGGTATC 125
Qy 1196 agctcaactcaagagcggtataatcgttaccagaatacaaggagataagcaggaagaa 1255
Db 126 AGCTCACTCAAAAGCGGTATATACGTTATCCACAGATCAGGGGATACGACAGAAAGA 185
Qy 1256 catgtgagcaaaaagcccaaaaagccaggaacgtaaaaagccgctgttgccgtt 1315
Db 186 CATGTAGCAAAAAGCCAGCAAAAAGCCAGAAACCTTAAAAAGCCCGCTGTGCGCTT 245
Qy 1316 ttccataagctcgcgcgccttcagcagatcacaaaalcgagctcgaagtcagagtg 1375
Db 246 TTTCCATAGGCTCCGCCCTCAGCAGCATCAAAAATCGACGCTCAAGTCAGAGGTG 305
Qy 1376 gegaaccccgacaagactataaagatacaagcggttcccccgtgaagctccctgtg 1435
Db 306 GCGAAACCCGACAGGACTATAAGATACAGGCGTTCCCTCGGAAGCTCCCTCGTGC 365
Qy 1436 ctctcctgttcgagacctgcggttacggataccctgttcgcttcccttcggggaag 1495
Db 366 CTCTCCTGTTCGACCTGCGCTTACCGGATACGTGTCGCTTCTCCCTTCGGGAAG 425
Qy 1496 cgtgcgcttctcactgaatgcacgctgtagtaccagttcgtgtgtagtgcgtc 1555
Db 426 CGTGGCGCTTTCATAGCTCAGCTGATAGTATCTCAGTTCGGTGTAGTCTGTTGCTC 485
Qy 1556 caagctggcgtgtgtgcacgaaccccccggttcagccgacgctgcgcttaccgtca 1615
Db 486 CAAGCTGGCGCTGTGTACAGAACCCCCCGTTACGCCGACCGCTGCGCTTATCCGTTA 545
Qy 1616 ctatgcttgcgtgaacacccggtlaagacagcctatgcacgtgcgcttcgacgactg 1675
Db 546 CTATGCTGTGATCCACCCCGGTAAACACGACTTATGCGCACTGACGACCCACTGG 605
Qy 1676 taacagattagcagagcagagtgtagcggtgtctacagaagttctgaagtgtgtgc 1735
Db 606 TAACAGATTAGCAGAGCGAGGTATAGCGGCTGTCTACAGATTTCTTGAAGTGTGGCC 665
Qy 1736 taactacgctacactaagaagacagatttggtatctgcgtcgtcgtca 1785
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RESULT 7

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AL656688 707 bp mRNA linear EST 13-DEC-2001
LOCUS AL656688 XGC-neurula silurana tropicalis cDNA clone TNeu032h21 5',
DEFINITION mRNA sequence.
ACCESSION AL656688
VERSION AL656688.1 GI:17669128
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 707)
AUTHORS Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu032h21.sp6

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QY 1636 cggtaagacagcattatcgccactgagcagccactgttaacagattagacagcga 1695
 DB 361 cggtaagacagcattatcgccactgagcagccactgttaacagattagacagcga 420
 QY 1696 ggtatgtaagcgggtgctacagagttcttaagtgtgtgacctactacagcagcaga 1755
 DB 421 ggtatgtaagcgggtgctacagagttcttaagtgtgtgacctactacagcagcaga 480
 QY 1756 ggaacagatttggatctgctgctgctgctgctgctgctgctgctgctgctgctg 1815
 DB 481 ggaacagatttggatctgctgctgctgctgctgctgctgctgctgctgctgctg 540
 QY 1816 gctcttgatccggcaaacacacacacacacacacacacacacacacacacacac 1875
 DB 541 gctcttgatccggcaaacacacacacacacacacacacacacacacacacacac 600
 QY 1876 agattacgcgcagaaaaaagagatcctcaagaagatccttcttcttcttcttctg 1935
 DB 601 agattacgcgcagaaaaaagagatcctcaagaagatccttcttcttcttcttctg 660
 QY 1936 agcttcagtggaagcaaaactacgttaaggaatttggatcagcagacatacttg 1995
 DB 661 agcttcagtggaagcaaaactacgttaaggaatttggatcagcagacatacttg 720
 QY 1996 aatgtattaga 2007
 DB 721 tctttacactaga 732

RESULT 9

AL635845 705 bp mRNA linear EST 12-DEC-2001
 LOCUS AL635845 XGC-neurula Silurana tropicalis cdna clone TNeu015d11 5',
 DEFINITION mRNA sequence.
 ACCESSION AL635845
 VERSION AL635845.1 GI:16787824
 KEYWORDS EST.
 SOURCE western clawed frog.
 ORGANISM Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Silurana.
 1 (bases 1 to 705)
 Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (10_2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Huckle E
 Sanger Centre
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: TNeu015d11.sp6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 location/Qualifiers
 1..705
 /organism="Silurana tropicalis"
 /db_xref="taxon:8364"
 /clone="TNeu015d11"
 /clone_lib="XGC-neurula"
 /dev_stage="neurula"
 /lab_host="Escherichia coli DH10B"
 /note="vector: pCS107, Site_1: EcoRI; Site_2: NotI; cdna
 was oligo dt primed from 5ug of poly A+ RNA from neurula.
 EcoRI-NotI cut cdna was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT 152 a 205 c 193 g 155 t
 ORIGIN

Query Match 8.6%; Score 698.6; DB 9; Length 705;

Best Local Similarity 99.4%; Pred. No. 3, 1e-163;
 Matches 701; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1079 gctgcaataatgaatcgcccaacgcgcgggagagcggttgcgtatgtggcgtcttc 1138
 DB 1 gctgcaataatgaatcgcccaacgcgcgggagagcggttgcgtatgtggcgtcttc 60
 QY 1139 cgtcttcctgcttactgactgctgctgctgctgctgctgctgctgctgctgctgctg 1198
 DB 61 cgtcttcctgcttactgactgctgctgctgctgctgctgctgctgctgctgctgctg 120
 QY 1199 tcaactaaagcggtataatcggtatccacaagaatacgaaggataacgaagaaacat 1258
 DB 121 tcaactaaagcggtataatcggtatccacaagaatacgaaggataacgaagaaacat 180
 QY 1259 gtgaagcaaaagcgcaaaagcgcaaaagcgcaaaagcgcaaaagcgcaaaagcg 1318
 DB 181 gtgaagcaaaagcgcaaaagcgcaaaagcgcaaaagcgcaaaagcgcaaaagcg 240
 QY 1319 ccaatagctcgccccctgagcagatcaaaaataatgagctcaagtcagaagtgagc 1378
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 DB 301 aaacccgacagactataaagatacagcagcgtttcccttggaagctcctcgtgcgc 360
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 DB 361 tccgttcgcacccctgcgccttaccggaatacctgtcgccttcccttcgggaagcgt 420
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 DB 421 ggcgccttctcaatgctcagcgtgtagatcctcaagtcagtcgtgtagtcgttcgca 480
 QY 1559 gctgggctgtgtgcagaaaccccccgcttcaagccgacgcgcgtcgtcgttaccgta 1618
 DB 481 gctgggctgtgtgcagaaaccccccgcttcaagccgacgcgcgtcgtcgttaccgta 540
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 QY 1679 caggaatgacagagaggtatgtagcggtgctacagagttcttgaagtgtgagctaa 1738
 DB 601 caggaatgacagagaggtatgtagcggtgctacagagttcttgaagtgtgagctaa 660
 QY 1739 ctacggctacactagaagacagatttggatctgctgcttgcct 1783
 DB 661 ctacggctacactagaagacagatttggatctgctgcttgcct 705

RESULT 10

AL643164 705 bp mRNA linear EST 12-DEC-2001
 LOCUS AL643164 XGC-neurula Silurana tropicalis cdna clone TNeu017ml3 5',
 DEFINITION mRNA sequence.
 ACCESSION AL643164
 VERSION AL643164.1 GI:16795289
 KEYWORDS EST.
 SOURCE western clawed frog.
 ORGANISM Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Silurana.
 1 (bases 1 to 705)
 Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (10_2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Huckle E
 Sanger Centre
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk

Db 301 TTATCCGTAACATATCTGTTGAGTCCAAACCGGTAGACACGACTTATGCCACTGGCA 360
Oy 1665 gcaagcactggttaacagagattagcagagcgaagtatgtaggcgtgtctacagaattcttg 1724
Db 361 GCAGGCACTGGTACAGAGGTTTAGCAGAGGAGGATGTAGGGGGGTCTACAGAGTCTTG 420
Oy 1725 aagtggtgacttaactagcgtctacactagaagaacagatattgtgtatctgctgctgctg 1784
Db 421 AAGTGTGGCTTAACCTAGCGGTACACTAGAACAGATTTGGTATCTGGCCTCTGCTG 480
Oy 1785 aagcagatcacttcggaagaaagatgtgtagctcttgatccgcgaacaacacccgct 1844
Db 481 AAGCAGATTACCTTCGGAAAAAGAGTTGTACTCTTGTCCGGCAACCAACCCAGCT 540
Oy 1845 gtagcagtggtttttttgtttgttgcaagcagcagattacgcggaagaaaaagatctaa 1904
Db 541 GGTACGGGTGGTTTTTGTGTGCAAGCAGCAGATTACCGCGAGAAAAAAGATCTCAA 600
Oy 1905 gaagatccttgatcttcttctacgaggtcgtgacgtcagctggaacgaacacagctaa 1964
Db 601 GAAGATCCTTGATCTTTTCTTACGGGGTCTGACGCTCAGTGAACGAAACTCAGCTTA 660
Oy 1965 gggatttggtcagcagcgatataattgaatgattaga 2007
Db 661 GGGATTTGTGTCATGATATCAAAAAAGATCTTCACTAGA 703

RESULT 15
AL636713 675 bp mRNA linear EST 12-DEC-2001
LOCUS AL636713 XGC-neurula silurana tropicalis cDNA clone TNeu013j03 5',
DEFINITION mRNA sequence.
ACCESSION AL636713
VERSION AL636713.1 GI:16788692
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
Xenopodinae; Silurana.
1 (bases 1 to 675)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu013j03.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
FEATURES
Source Location/Qualifiers
1..675
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu013j03"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into PCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 160 a 187 c 179 g 149 t
ORIGIN

Query Match 8.2%; Score 669.2; DB 9; Length 675;
Best Local Similarity 99.6%; Pred. No. 6.9e-156;
Matches 671; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1201 actcaaaaggcgttaatacgttataccacagaatcaaggagataacgcaggaagaaacatgc 1260
Db 2 ACTCAAAAGCGGTAAATACGTTATCCAGAAATCAAGGGATTAACGAGAAAGAACATGT 61
Oy 1261 gaggcaaaagccagcaaaaagccaggaacccgtaaaaaggccggtgtcgtgctgtttcc 1320
Db 62 GAGCAAAAAGCCACAGCAAAAAGCCAGGAAACCGTAAAAAGCCCGCTGTGCGGTTTTC 121
Oy 1321 ataggtccgcccccttgccagatcatcaaaaatcgaagctcaagtcgaagtgtgcga 1380
Db 122 ATAGGCTCCGCCCTTGACGAGCATCAAAAAATCGAGCTCAAGTCAAGAGTGCGGA 181
Oy 1381 acccgacaagactataaagataccaggcgtttcccccgtgaagctccctcgtgcgtc 1440
Db 182 ACCCGACAGGACTATTAATACAGAGCTTTCCTCCCTGGAAGTCCCTGTCGCTC 241
Oy 1441 ctgttcgacccctgcgcgttacccgatacctgttcgccttctccctcgtggaaagcgttg 1500
Db 242 CTGTTCCGACCTGCGCGTTACCGGATACCTGTCGCCCTTCTCCCTCGGGAAGCTGG 301
Oy 1501 cgtcttctaagtctcagcgtgtgaagtaactcagttcgtgtgaagtgtcgtcccaagc 1560
Db 302 CGCTTCTCATAGCTACAGCTGAGGTAGTCTAGTGGTGAAGTCTTCCTCCCAAGC 361
Oy 1561 tggcgtgtgtgcaagcaaccccccgttcaagccgacccgtgcgcctatccggttaactac 1620
Db 362 TGGCGTGTGTCACGACACCCCGCTTACGCCGACCGCTGCGCTTATCCGTAATATC 421
Oy 1621 gcttgaagtcacacccggtgaagacacgactatcgccactggaagcagcactgtgtaac 1680
Db 422 GTCTGAGTCCAAACCCGTAAGACACAGACTATTCGCCACTGGCAGCAGCAGCTGTAA 481
Oy 1681 ggttaagcagcagcaggtatgtgaagcgtgtcactaagagttcttgaagtgtgtgctaa 1740
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Oy 1741 acggtacactagaagaagacagatattgtgatactgcgctgtctgtaagccagttactcg 1800
Db 542 ACGGCTACACTGTAAGAAACAGATTTGATCTGGCGCTGTGTAAGCCAGTTACTCTTG 601
Oy 1801 gaaaaagagtgtgtagctctgtatccggcaaaaacacacgcgtgtgtagcgtgtgttt 1860
Db 602 GAAAAAGAGTTGTAGCTCTTGATCCGGCAAAACACCCGCTGTGACGGGTGTTT 661
Oy 1861 ttgtttgcaagcag 1874
Db 662 TTGTTTGCAGCAG 675

Search completed: May 24, 2002, 07:54:33
Job time: 24800 sec

